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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 12, 2003, 20:06:02; Search time 18 Seconds (Without alignments) 856:931 Willion cell updates/sec UG-10-084-700-2 1772SNEFKLNQPPEDGISSV......DGIFIRQVTDAETKPKSPCT 328 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by charce to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries SwissProt_41:* Database :

SUMMARIES

		Description			P40066 saccharomyc	P41838 schizosacch	P78406 homo sapien	Q93454 caenorhabdi		-	Q8yril anabaena sp	OBytc2 anabaena sp	thermomon													-		P25387 chlamydomon	-			Q09715 schizosacch	•	leishmani	Q8yv57 anabaena sp
SUMMAKIES	,	ΙD	BUB3 HUMAN	BUB3 MOUSE	YET7 YEAST	RAE1_SCHPO	RAIL HUMAN	YSAK CAEEL	BUB3 YEAST	RAIL ARATH	YY46 ANASP	YSOO ANASP	PKWA THECU	GBB2_CAEEL	HET1 PODAN	PRL1 ARATH	YH92_CAEEL	GBB1 RAT	WDR1 CHICK	GBB1_HUMAN	T2D4_HUMAN	PWP2 SCHPO	PRL2_ARATH	WDR1_XENLA	GBLP_ARATH	GBLP_TRYBB	PR17 YEAST	GBLP CHLRE	RCO1 NEUCR	YJL2 YEAST	GBLP_LEICH	TU11 SCHPO	W146_HUMAN	GBLP_LEIMA	YL24 ANASP
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		Match Length	328	326	365	352	368	373	341	251	1526	1258	742	356	1356	486	501	340	609	340	800	854	479	609	327	318	455	318	604	714	312	614	1336	312	1683
	Ouerv	Match	100.0	98.4	30.4	28.9	28.7	23.6	20.1	19.9	12.9	11.8	11.1	10.0	6.6	9.9	9.8	9.7	9.6	9.6	9.6	9.6	9.5	9,5	9.5	9.4	9.4	9.4	9.4	9,3	9,3	9.3	9.3	9.5	9.5
		Score	1772	1743	538	511.5	509	418.5	356	352.5	228	209	197.5	177.5	176	175.5	173	171.5	170.5	169.5	169.5	169.5	169	169	168.5	167	167	166	166	165.5	164.5	164.5	164	163.5	163.5
	Result	%	7	0	e	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	58	59	30	31	32	33

0 nicotiana p	6 nicotiana t	7 bos taurus	9 xenopus lae	6 homo sapien	0 homo sapien	8 dictyosteli	4 biomphalari	5 caenorhabdi	6 medicago sa	6 glycine max	3 caenorhabdi
P9334	P4902	P1101	p79959	P1101	09hav	P906d	09313	Q2121	02407	03983	P1734
GBLP NICPL	GBLP_TOBAC	GBB2_BOVIN	GBB1_XENLA	GBB2_HUMAN	GBB4 HUMAN	KMHB_DICDI	CBLP_BIOGL	GBLP CAEEL	GBLP-MEDSA	GBLP_SOYBN	GBB1_CAEBL
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326	326	326	340	340	340	732	316	324	325	325	340
9.5	9.1	9.1	9.1	9,1	9.1	9.1	0.	9.0	6.8	6.8	6.8
162.5	161.5	160.5	160.5	160.5	160.5	160.5	160	160	158.5	158.5	158.5
3.4	35	36	37	38	39	9	4	42	43	44	45

ALIGNMENTS

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BUB3_MOUSE
                                                    RESULT 2
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                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BWBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute. Swiss and the Swist content was by moneyit institutions as long as from each content is no use modified and this statement is not removed. Usage Am of for commercial entities requires a license agreement (see http://www.isb-sh.ch/Ammounce/or send an enail to license@ibe-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SFHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYMYB 300
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Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schrein J.S., Mones S.J.M., Merze M.S., Gener A., Schrein J.S., Olones S.J.M., Merze M.S., Werker and Charles J. S. S., Merze Han 15,000 full-length human and mouse charles sequences **, 1589-11800 (2002)

P. F. PHOTON: ROUNTS DUTKINGOONES LOCALIZATION OF BUB1.

** SUBDILLY INTERACTS WITH BUB1 AND FURST.

** SUBDILLY INTERACTS WITH BUB1 AND LOCALIZATION OF BUB1.

** SUBDILLY INTERACTS WITH BUB1 AND LOCALIZATION OF BUB1.

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; Pred. No. 5.9e-146;
0; Mismatches 0; Indels 0;
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2915572A57368E5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005699; C:kinetochore; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0007067; P:mitosis; TAS.
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PROSITE; PS50081; WD REPEATS 2; 2.
PROSITE; PS50294; WD REPEATS RRGION; 1.
Nuclear protein; Repeat; WD repeat.
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ProDom; PD000018; WD40; 1.
SMART; SM00320; WD40; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF047472; AAC28438.1; -. EMBL; AF053304; AAC06258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF081496, AAC36307.1; -. EMBL, AF047473, AAC364139.1; -. EMBL, BC005138; AAH05138.1; -. EMBL, BC022438; AAH22438.1; -.
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Best Local Similarity 100.0
Matches 328; Conservative
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223
326
326
328 AA;
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AC ONVALOR DELABORS STANDARD, PRT, 136 AA.

AC ONVALOR (Rel. 23). Created DELABORO (Rel. 24). Last sequence update)

BY ALTOSONO (Rel. 24). Last sequence update DELABORO (Rel. 27). Last sequence update DELABORO (Rel. 27). Last sequence update DELABORO (Rel. 27). Last sequence DELABORO (Rel.
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Gabs

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63 AFY--DPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEY--CPEVNV--MVTGSW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 TRWSNDGTKVASGCCDNALKLYDIASGCTQOGGMHSAPIKVLRFVQCGPSNTECIVTGSW 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 DQIVKLWDPRIPCNAGIFSQPEKVYTLSVSGDRLIVGIAGRRVLVWDLRNMGYVQQRRES 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 INIEQIYPVNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASL---AFS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 NGOSLVYPVNSIAFHPLYGTFVTAGGDGTFNFWDKNORHRL---KGYPTLQASIPVCSFN 320
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                                                                                                                                                                                                                                                                                                                               4 SNEFKINQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQH-TGAVLDC 62
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                                                                                                                                                                                       30.4%; Score 538; DB 1; Length 365; 35.7%; Pred. No. 3.7e-39; Live 59; Mismatches 135; Indels 26;
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Brown J.A., Bharathi A., Ghosh A., Whalen W., Fitzgerald E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 NDGTTLAIASSYMY---EMDDTEHPEDGIFIROVTDAETKPK 324
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34 74 WD 1.
78 117 WD 2.
119 162 WD 3.
129 164 WD 3.
365 AA, 40822 WA, 3FSB201EB1BAEEG CRC64,
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Schizosaccharomyces pombe (Fission yeast)
Schizosaccharomycetales; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaces;
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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RAEL OR SPBC16A3.05C,
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                                                                                                                                   121 KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLWNWGYVQQRRESSLKY 180
                                                                                                                                                                                                       QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI 240
                                                                                                                                                                                                                                           181 OTRCIRAFDNKOGYVLSSIEGRVAVEYLOPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI 240
                                                                                                                                                                                                                                                                                                                                    SFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
                                                                                                                                                                                                                                                                                                                                                                         241 SFHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
     61 DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication F. S., Walligan J.T., Hennessy K.M., Yolton M.A., Allen E., Acario R., Aviles B., Berno A., Bernan T., Carpenter J., Chen E., Acario R., Aviles B., Berno A., Bernan T., Carpenter J., Chen E., Hunides-Earl G., Hartezh G., Handides-Earl B., Mosera A., Koon C., Labakkari D., Lee H., Hunides-Earl B., Makhahaz K., Nanah A., Norgen R., Cefner P., On C., Pett P., Koon C., Pett M., Carpett P.K., Roberts D., Sohats M., Norgen R., Cefner P., Real H., Taylor P., Wel Y., Spettsin D., Novis R.M., Mark M., Taylor P., Wel Y., Spettsin D., Novis R.M., Mark M., Araylor P., Wel Y., Spettsin D., Novis R.M., Mark M., Carlin M., Araylor R., Mark M., Ma
                                                                    KLMDPRIPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLWDLRNMGYVQQRRESSLKY
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-!- SIMILARITY: CONTAINS 4 WD repeats.
-!- SIMILARITY: BELONGS TO THE RAEI FAMILY OF WD-REPRAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Puigi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomyces.
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0.78E-1995 (Ral. 10, last sequence update)
11-58E-2003 (Ral. 42, last amovation update)
Mpotherical 40.5 Ken TEP-abp repeats containing procein in NIP159-7pHS integrant Festion.
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PROSITE; PSS00081; WD_REPEARS_21, 4.
PROSITE; PSS0294; WD_REPEARS_REGION; 1.
Hypothetical protein; Repeat; WD_repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 MDDTEHPEDGIFIRQVTDAETKPKS 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 MDDTEHPEDGIFIROVIDAETKPKS 325
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SMART; SM00320; WD40; 4.
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298 --- MYEMDDIEHPEDGIFIRQVIDAETKPK 324 319 WSKGYTFNNAOLP-NKIMLHPVPQDEIKPR 347

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As woodward J., Volckeert G., Aert R., Robben Je, Grymonpers B.,
As weltjens I., Vanstreels ar. Raegar Mr. Schneed Mr. Malbart Hus S.,
As dabe C., Paths M., Prick G., Lobrach H., Rollabert Hus S.,
As dabe C., Paths M., Prick G., Lobrach H., Rollabert H. Pohl T.M.,
As Garren K. Zimesonn M. Roddler M., Marbutt R., Parinelle B.,
As Gaffeart P., Ares S.J., Kang Z., Hull C., Moore K., Hurst B.,
As Lobrach M., Rochet M., Galllardin C., Tallada V. A., Garron A., Thode G.,
As Dominger A., Revuelta J.L., Moreno S., Armstrong J., Porsburg S.L.,
As Shpakovski G.V., Ussery D., Bartel M., Bolts Mr. P., Balico J.,
As Shpakovski G.V., Ussery D., Bartel M., Polesskin J.,
Weller H., John T., Woodmin M., Moreno S., Armstrong J., Porsburg S.L.,
As Shpakovski G.V., Ussery D., Bartel M., Bolts Mrae P., In Possakkin J.,
Weller J., All St. Brit. Beller B., Mrae P., In Head B.,
Weller B., All St. Brit. Bolts Mrae P., In Head B.,
Weller B., All St. Brit. Bolts Mrae P.,
Weller B., All St. Brit. Bolts Mrae P., In Marker B.,
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28.9%; Score 511.5; DB 1; Length 352;
Begt Local Skimllarity 34.8%; Pred. No. 76-97.

Matches 115; Conservative 58; Mismatches 142; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whalen W.A., Bharathi A., Danielewicz D., Dhar R., "Advancement through mitosis requires rael gene function in fission
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PITA ASG11.

OGNOBOL SEPACE 195.7 No.-

CONTROL SEPACE 195.7 No.-

PRINTS. PROMOTION, ORGANIZEDRAT.

REMARY. SHOROZON, WANG. P. 18.

REMARY. P. 10.

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1.13 1.05 NO. 5.

1.14 NO. 5.

TREMPERAT.

1.15 NO. 5.

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EMBL, AL021748, CAA16856.1; -.
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Yeast 13:1167-1179(1997),
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Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens (Human).

NCBI TaxID=9606;

priston Corp. Sec. Adulto's Copyles.

11-ULT-1998 [RE1. 34] Created)

11-ULT-1998 [RE1. 34] Created)

11-ULT-1998 [RE1. 34] Late amocarion update)

mRNH-secoiated protein mrnp 41 (RAEI protein homolog).

PRT; 368 AA.

STANDARD,

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BEOURNE FROM THE STATE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with human RAE1 gene is a functional homologue of Schizosaccharomyces nombe rael gene involved in nuclear export of poly(A)+ RNA.";
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BINDS MRNA. MAY FUNCTION IN NUCLEOCYTOPLASMIC TRANSPORT AND IN DIRECTLY OR INDIRECTLY ATTACHING CYTOPLASMIC MRNPS TO THE
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"The DRA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bharathi A., Ghosh A., Whalen W.A., Yoon J.H., Pu R., Dasso M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97464358; PubMed-9256445;
Kacher II, B. Blobein Gri
Fark binding protein Gri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roc. Natl. Acad. Sci. U.S.A. 94:9119-9124(1997).
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its $8158.PROT entry is copyright. It is produced through a collaboration between the Suisa Three-three of Bioinformatics and the Regio currention. There are no restrictions on its broppen Bioinformatic institute. There are no restrictions on its many profit control as a long as its content in in no way many profit and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an enail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 GAVLDCAFY-DPTHAWSGGLDHQLKMHDLNTDQENLVCTHDAPIRCVEYCPEVN----V 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 MVTGSWDQTVKLWDPRTPCNAGTFSQ---PEKVYTLSVSGDRLIVGTAGRRVLVWDLRNM 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TGSNEFKLNOPPEDGISSVKFSPNTSQ--FLLVSSWDTSVRLYDV-PANSMRLKYQHT-- 56
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                           -2010-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Mypothetical 41.4 kba 71p-Asp repeats containing protein F10G8.3 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: CONTAINS 4 WD repeats.
-i- SIMILARITY: BELONGS TO THE RAE! FAMILY OF WD-REPEAT PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Mismatches 145; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Basham V.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 AA; 41413 MW; BOB151DB47FC3526 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . No. 8.3e-29;
                                                                 373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROGRAFIE 1 950009 1 WD REPERS 1 2 PROGRAFIE 1 950009 1 WD REPERS 1 950009 1 WD REPERS 1 950009 1 WD REPERS 1 950000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1 95000 1
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23.6%; Score 418.5;
Best Local Similarity 31.5%; Pred, No. 8.3
Matches 109; Conservative 63; Mismatches
                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPRO01660; WD40.
Pfam; PP00400; WD40; 4.
PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z80216; CAB02280.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MormPep; F10G8.3; CE09338.
                                                                 STANDARD;
                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                  (Rel. 36, (Rel. 36, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T20723; T20723.
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                            chromosome I.
                                                                                                                  15-JUL-1998
                                                                                                                                       5-JUL-1998
                                                             YSAK CAEEL
Q93454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                 F10G8.3
    KESULT 6
YSAK CAREL
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                                                                                                                      is SWISS-PROT with the solutions of the swiss produced through a collaboration between the swiss include of Bioinformatics and the SMBO dustaction—the Burgean Boileformatics and the SMBO dustaction—the Burgean Boileformatics and space are no restrictions on its use by more profit in the space of the statement the statement of the statement of the space o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 QTVKLMDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 BFKLNQPPEDGISSVKFSPNT--SQFLLVSSWDTSVRLYDVPANSM---RLKYQHTGAVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 LKYQTRCIRAFPNKQ----GYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 - BQIYPVNAISFHNIHNTFAIGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTT
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                                                 SIMILARITY: Contains 4 WD repeats. SIMILARITY: BELONGS TO THE RAE! FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.7%; Score 509; DB 1; Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 34.3%; Pred. No. 1.2e-36;
Matches 116; Conservative 61; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89A99C34BA668A97 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             F -> L (IN REF. 2).
D -> G (IN REF. 2).
F -> S (IN REF. 2).
T -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                           U85943; AAC20127.1;
AL135939; CAB99471.1;
AL109955; CAC21461.1; -..
HGNC:9828; RAEI.
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                                                                                                                                                                                                                                                                                                                                       EMBL; U84720; AAC28126.1; -.
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31
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158 1
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CONFLICT
SEQUENCE
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EMBL, A
EMBL, A
Genew,
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281 SLAFSNDGTTLAIASSYMYEMDDTEHPEDG---IFIRQVTDAETKP 323

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                                          104 ICRICKYGDDKIAASWDGLIEVIOPRNYGDGVIAVKNLNSNNTKVKNKIFTMDTNSSRL 163
                                                                                                                                             151 IVGTAGRRVLVWDL----RNWGYVQQRRESSLKYQTRCIRAFPNKQ-GYVLSSIEGRVAV 205
                                                                                                                                                                                                    164 IVGMANSQVQMFRLPLCEDDNGTIE---ESGLKYQIRDVALLPKBQEGYACSSIDGRVAV 220
                                                                                                                                                                                                                                                                                                            206 EYLDPSPE--VQKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNTFAIGGSDGFVNIWDP 263
                                                                                                                                                                                                                                                                                                                                                                          221 BFFÖDGGDDYNSSKRFAFRCHRINLKDTNLAYPVNSIEFSPRHKFLYTAGSDG11SCWNL 280
111 ------MVTGSWDQTVKLWDPRT-----PCNAGTFSQPEKVYLLSVSGDRL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: Contains 4 WD repeats.
-i- SIMILARITY: BELONGS TO THE RAEI FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A 37.5 Xb sequence from Arabidopsis thaliana chromosome I.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
Goodman H.M., Gallant P., Keifer-Higgins S., Rubenfield M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 OTRKKIRNPAKFNEDSVVKIACSDN--ILCLATS-----DDT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 FNKKRLCQFHRY-PTSIASLAFSNDGTTLAIASSYMYEMDDT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U53501; AAA98915.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAIL ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 CAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYC------PEVNV- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CNFID...------NTDLQIYVGTVQGBILKVDLIGSPSFQALTNNEANLG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S QIEQAPKDYISDIKIIPSKS-LLLITSWDGSLTVYKFDIQAKNVDLLQSLRYKH--PLLC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 KLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLY--DVPANSM----RLKYQHTGAVLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91330299, PubMed=1651171,
MEDLINE=91330299, PubMed=1651171,
T. cerevishe genes required for cell cycle arrest in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S. M. Marise A.C., Grivell L.A.;
Ge Haan M., Maarse A.C., Grivell L.A.;
Manitted (MAT-1995) to Che EMBL/GenBank/DDBJ databases.
-- FUNCTION: REQUIRED FOR CELL CYCLE ARREST IN RESPONSE TO LOSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWART; SWOOZÓ, WANO, SP
PROSTES PROCESTES PROC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast)
Bukaryota; Impgi, Ascomyoota; Saccharomyotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 341;
            325 CCDVHSSGAFLVYALGYDWSRGHEGNTQPGSKIVIHKCIEDMKPRP 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBDFB8697935BCEB CRC64;
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                                                                                                                                                                                                                                                                       01-AVG-1992 (Rel. 2). Created)
ALGU-1992 (Rel. 2). Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
BUB3 OCT I rocle arrest procein BUB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SUBCELLULAR LOCATION: Nuclear (Probable).
-:- PTM: PHOSPHORYLATED BY BUB1.
-:- SIMILARITY: Contains 3 WD repeats.
                                                                                                                                                                                                    341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005699; C:kinetochore; IPI.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 3.
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1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            loss of microtubule function.";
Cell 66:507-517(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M64707; AAA34459.1; -.
EMBL; X87331; CA60742.1; -.
EMBL; Z74934; CAA99216.1; -.
PIR; B39654; B39654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF MICROTUBULE FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103; Conservative
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S0005552; BUB3
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Best Local Similarity
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Matches
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75 LDHQLKMHDLWTDQ-ENLVGTHDAPIRCYEYCPEVNVMVTGSWDQTVKLWD----- 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 RLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRAFP-NKQGYVLSSIEGRVAVEY 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1130 TLANGSSDQIVRLWDISS-----KKCLYTLQGHTNWVNAVAFSPDGATLASGSGDQIVRL 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1185 WDIS-----SSKCLYILQGHTSW---VNSVVFNPDGSTLASGSSDQTVRLWSINSSK 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 LDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNTFATGGSDGFVNIWDPPNKK 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 ISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDCAF-YDPTHAWSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1010 GDQTVRLWDISSSQCFYIFQGHTSCVRSVVFSSGGAMLASGSDDGTVRLWDISSGNCLYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.9%; Score 228; DB 1; Length 1526; 25.8%; Pred, No. 1.6e-11;
                                                                                                                                                                                                                              PERION, PROGRAMMENT.
PERIONS, PROGRAMMENT.
PETCOME, PRODOCOLS, HONG, 13.
PROGRIFE, PROSCO'SE, MOR PERENTS, 1.1.
PROGRIFE, PROSCO'SE, MOR PERENTS, 2, 15.
PROGRIFE, PROSCO'SE, MOR PERENTS, 2, 15.
PROGRIFE, PROSCO'SE, MOR PERENTS, PROGRAMMENT, PROGRIFE, PROSCO'SE, MOR PERENTS, PROGRAMMENT, 134, 175, MOLTING, PROGRAMMENT, PROGRAMMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Mismatches 121; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1234 CLCTFOGHTSWVNSVVFNPDGSMLASGSS 1262
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PENTAPEPTIDE.
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                   send an email to license@isb-sib.ch)
                                                                                                                                     Interpro, 198001646; Speptide repeat.
Interpro; IPR007111; NACHT NTPase.
InterPro; IPR001680; WD40.
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WD 13
WD 15
WD 15
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                                                      EMBL; AP003593; BAB75165.1; -. PIR; AC2239; AC2239.
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Machania M., Ziigouli M., Ishkawa A., Kasashima K., Kimiza T.,
Mandanaki M., Shingo S., Sugimoto M., Mateuno A., Muraki A.,
Mandanaki M., Shingo S., Sugimoto M., Takazawa M., Yamada M.,
Mandanaki M., Shingo S., Sugimoto M., Takazawa M., Yamada M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WDQTVKLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNNGYVQQRRE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 PVLCSAWKDDGTTVFSGGCDKQAKMWPLLSGGQPVTVAMHEGPIAAMAWIPGMNLLATGS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 SSLKYQTRÇIRAFPNKQGY--VLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 SNEFKLNQPPEDGISSVKFSPNTSQPLLVSSWDTSVRLYDVP-----ANSMRLKYQHTG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 NKSYEVTPSPADSISSLSFSPR-ADILVATSWDNQVRCWEISRSGASLASAPKASISHDQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.9%; Score 352.5; DB 1; Length 2: 30.8%; Pred. No. 2.5e-23; ive 45; Mismatches 87; Indels
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Bacteria, Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_HAXID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   397E80AC66DE24DF CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last semocation update)
Hypothetical MD-repeat protein alr3466.
BREM. ACCUTATI, AMPI-4654.1; ...
PIR; ST1241, ST7241.
Intereptor, IRROMAGO, BROWNING.
PEARNY, SPROADO, PROFESTIENBEPT.
SPARKT, SKO0320, WAGG, 4.
SPARKT, SKO0320, WAGG, 4.
PROSITE, PSE00524, WAGG, 8.
PROSITE, PSE0054, WAGG, 8.
PROFESTION, 1.
PROFESTION, WAGG, 9.
PROFESTION, W
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MEDLINE=21595285, PubMed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                        88
8.4
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153 1
251 AA;
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Q8YRI1,
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1069

66; Gaps

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This swiss-rayor entry is copyright. It is produced through a collaboration between the Swiss Institute of Boinformatics and the EMBL outstation the EMPLOADED SWISSELL OF SWI
                                                                                                                                                                                                                                           1007 ISTGQCFQILLEHIDWY---AVVFHPQGKIIATGSADCTVKLWNISTGQCLKTLSEHSD 1063
                                                       222 ----KCHRLKENNIEQIYPVNAISFHNIHNTFATGGSDGFVNIMDPPNKKRLCQFHRYPT 277
172 ORRESSLKYQTRCIRAFPNKQGYVLSSIEGRVAVEY-LDPSPEVQKKKXAF----- 221
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- Faretrion, 179:1897 18911998)
- Faretrion, May Far An Regillaringon Role Durino Hue Conclets Growth CYCLE AND IN SECONDAR METABOLITE PRODUCTION.
- CATALYTIC ACTUAT: AFT A procein = ADP • a phosphoprocein.
- SAMLANTY SELOWES TO THE SER/HR FAMILY OF PROTEIN KINSES.
- SHILLARITY EDLOWES TO THE SER/HR FAMILY OF PROTEIN KINSES.
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PROSITE, SEGOLI, PROTEIN KINASE DAF, 1.

PROSITE, SEGOLI, PROTEIN KINASE DAF, 1.

PROSITE, SEGOLI, PROTEIN KINASE DAF, 1.

PROSITE, SEGORI, W. REPEKFE, 1, 5.

PROSITE, SEGORA, W. REPEKFE, 2, 5.

PROSITE, SEGORA, W. REPEKFE, 2, 5.

PROSITE, SEGORA, W. REPERFE, SEGION, 1.

THANGERASE, SECINA, 1.

THANGERASE, SECINA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Batteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptosporanginese, Thermomonosporaceae, Thermomonospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
14-SEP-2003 (Rel. 42, Last amnotation update)
Probable serine/threonine-protein kinase pkwA (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PRO/GLU/ASP-RICH (SPACER).
WD 1.
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WBDLANB-SCR0125, PubMed-8631732, Serricek M.,
Janaa L., Tichy P., Spisek J., Petricek M.,
Janaa L., Tichy P., Spisek J., Petricek M., Andering
"A deduced Thermomonospora curvata protein containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   742 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
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Interpro; IPR000719; Prot kinase.
Interpro; IPR002290; Ser Ehr_pkinase.
Interpro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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ProDom; PD000001, Prot kinase; 1.
ProDom; PD000018; WD40; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1064 KILGMAWSPDGQLLASASA 1082
                                                                                                                                                                                                                                                                                                                                                         278 SIASLAFSNDGTTLAIASS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00069, pkinase; 1.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermomonospora curvata.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKWA OR PKW1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
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24.5%; Pred. No. 5.4e-10;
.ive 60; Mismatches 139; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGISSVKFSPNTSQFLLVSSNDTSVRLYDV-PANSMRLKYQHTGAVLDCAF-YDDTHAWS
                                                                                                                                                                                                                                                                      where T. Where T. W. Welker E. W. Kaweshims K. K. Mursh T. W. Kakeshims K. M. Kimura T. W. Kakeshims K. M. Murshi A. T. Walida Y. Kohara M. Watsunde M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRODAZIO; GRPGAIZHRRRY.
PRODAZI, FORGOZIO; GRPGAIZHRRY.
SWART, SKOOZIO, HDQ. 14.
PROSITE; PSCOOZI, HDQ. 14.
PROSITE; PSCOOZI, HDQ. 14.
PROSITE; PSCOOZI, HD REPRING_2, 14.
PROSITE; PSCOOZI, HD REPRING_2, 14.
PROSITE; PSCOOZI, HD REPRING_2, 14.
PROSITE; PSCOOZI, SREPRING EXCOOZION; 1.
             Anabaena sp. (strain PCC 7120).
Benteria: 'Qanobateria: Nostocales; Nostocaceae; Nostoc.
Taxid-105690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139513 MW; 45DF03B91170C451 CRC64;
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PIR, AIZISS, AIZISS.
InterPro; IPR000758, DS-ARC.
InterPro; IPR001882, NB-ARC.
InterPro; IPR001680, WD40.
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                                                                                                                                                                                                                                           MEDLINE=21595285; PubMed=11759840;
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Pfam; PF00401; NB-RC; 1.
PRINTS; PR00364; UDSEASERSIST
PRINTS; PR00320; GPROTEINBRPT.
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1144 118
1186 122
1258 AA;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to licensc@isb-sib.ch).
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                                                                                   Wormpep, FS2A8.2; CE17845.
InterPro, IPR001632; Gprotein B.
InterPro, IPR001680; WD40.
                                     EMBL; AP291847; AAK55964.1; -.
                                                                                                                        PEAM: PFOOLOGY WOOD; 7.
PRINTS: PRO0320; GPROTEINB.
PRODOM; PRODOM; WOOD; WOOD
                                                                                                                                                                                                                                                                                                                            39453 MW;
                                                 , Z71263; CAA95824.1; -. T22478; T22478.
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                           SMART: SM00320; WD40;
                                                                                                                                                                                                                                                                                                                            356 AA;
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
tes 70; Conserv
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                                                                             HSSP: P04901; 17BG
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Matches
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HETI_PODAN
     SCREET TETE WAS BURNESS SON SERVICES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit. Institutions as long as its content is in no way modified and this statement is not removed. Usage by, and for commercial
                                                                                                                                                                                                       561 GSRDGTARLWAVATGTEHAVLKGHIDYVYAVAFSPDGSWVASGSRDGTIRLWDVATGKER 620
                                                                                                                                                                  502 DWVRAVAFSPD-GALLASGSDDATVRLWDVAARERRAVFEGHTHYVLDIAFSPDGSMVAS $60
                                                                                                                                                                                                                                         132 GTFSQP-EKVYTLSVSGD-RLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRAFP 189
                                                                                                                                                                                                                                                         621 DVLOAPAENVVSLAFSPDGSMLVHGSDSTVHLMDVASGEALH-----TFEGHTDMVRAVA 675
                                                                                                                                                                                                                                                                                        190 -NKQGYVLSSIBGRVAVBYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNT 248
                                                                                                                                                                                         73 GGLDHQLKWHDLNTDQENLV-GTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRTPCNA 131
                                                                                                                                                                                                                                                                                                                676 PSPDGALLASGSDDRIIRLWDVAAQBE-----HITLEGHTE---PVHSVAFHPEGTT 724
                                                                                                                                        15 DGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDCAFY-DPTHAWS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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WHO THORN THE ALM W. SIMMOR P. C. ONDRON B. P. DISRECK R.H.H.J. SEQUENCE "THE G PROCEED HORS SHAWING EDP-27 IN CHARDABACKIE & BAGGRAIN FEQUENCE FOR THE COLOR PLANT PROPERTY OF A PROCESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA AND GAMMA). Interacts with goal., ear-l6, egl-10, egl-30.
I- SUMILARITY: Connains 7 WD repeats.
                                                                                                                23;
                                                                                     11.1%; Score 197.5; DB 1; Length 742; 27.7%; Pred. No. 2.7e-09; ive 48; Mismatches 112; Indels 23;
                                                               AC1734640DB4383D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guanine nucleotide-binding protein beta subunit 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 356 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND INTERACTIONS.
   MD 5.
                                                                 78950 MW;
                                                                                                    1 Similarity 27.7%;
70; Conservative 4
                                                                                                                                                                                                                                                                                                                                          249 FATGGSDGFVNIW 261
                                                                                                                                                                                                                                                                                                                                                                 725 LASASEDGTIRIW 737
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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       539
581
622
664
706
742 AA;
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Q20636,
                                                                                        Query Match
Best Local
                                                                 SEQUENCE
     REPEAT
REPEAT
REPEAT
                                           REPEAT
                                                     REPBAT
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                                                                                                                  Matches
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83 IVSSSQDGKVIVWDGFTINKEHALIMPITWYMACAPSPSSQMIACGGLDNKCSVVPLSFE 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 DDIIQKKRQVATHTSYMSCCTFLRSDNLILTGSGDSTCAIWDVESGQLIQNFHGHTGDVF 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 TLSV----SGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRAFPNKQGYVLS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 AIDVPKCDTGNTFISAGADKHSLVWDIRSGOCVOSFEGHEADINT--VRFHPNGDAFATG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 SIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNTFATGGSDGF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 SDDATCRLFDLRADRQV-----CVYEKES---ILFFVNGVDFSLSGRILFAGYGDYR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 LLVSSWDTSVRLYD-VPANSMRLKYQHTGAVLDCAFYDPTHAWS-GGLDHQ----LKMH 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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SAUPE 5. Thrce B. . Bequeret b. Sequence and the fundamental for vegetative incompatibility in the fungus Podospora ansertine encodes a protein with a GTP-binding motif and G beta homologous domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae, Sordariales, Lasiosphaeriaceae; Podospora,
NKDL TAXID-5145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.0%; Score 177.5; DB 1; Length 356; 25.2%; Pred. No. 5.5e-08; Live 40; Mismatches 143; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293AA6DCF317D832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 UNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIAS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 VGVWDSLKCARHSVLYGHENRISCLRTSPDGTAVCSAS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00678; WD REPEATS_1; 3.
PROSITE; PS50082; WD REPEATS_2; 5.
PROSITE; PS50082; WD REPEATS_2; 5.
PROSITE; PS05294; WD REPEATS_REGION; 1.
Transducer; Repeat; WD repeat; Multigene family.
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last amrotation update)
Vegetalible incompatibility protein HET-E-1.
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486 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        947 HTIKIWDAASGTCTQTLEG-HGSSVLSVAPSPDGQRVASGSGDKTIKIWDTA----SGTC 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1047 LEGHGGWVQSVVF-----SPDGQRVASGSDDHTIKIWDAVSGTCTQTLEGHGDSV 1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HQLKMHDL--NTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRTPCNAGTF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 SQP----EKVYTLSVS--GDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 FPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAPKCHRLK------ENNIEQI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 YPVNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
                     -!- FUNCTION: RESPONSIBLE POR VEGETATIVE INCOMPATBILITY THROUGH SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED GENE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 SVKPSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDCAFY-DPTHAWSGGLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 1356;
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                                                                                                      -!- SIMILARITY: Contains 10 WD repeats.
-!- SIMILARITY: Contains 1 NACHT domain.
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    162:135-139(1995)
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                                                                       15-7UL-1998 [Rel. 15, Created)
15-8UL-1998 [Rel. 15, Created)
15-8UL-1999 [Rel. 15, Larg sequence update)
15-8UL-1990 [Rel. 14, Larg annotation update)
15-8UL-1900 [Rel. 14, Larg annotation update)
15-8UL-1902 [Rel. 17, Post phosphases pleater to response to the property of the propert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nemeth K., Putnoky P., Stankovic B., Bako L., Mathur J., Redei G.P., Schell J., Koncz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Gaps 16;
Sekton M., Murray J., Sheet P., Cordes M., Abu-Threadsh J.,
B. Sekton M., Murray J., Sheet P., Cordes M., Abu-Ta, Scott K., Johnson D.,
M. Hattesling, Coutting V., Cloud J., Abbort A., Scott K., Johnson D.,
M. Minx B. Benfley D. Fulton B., Miller M., Creco T., Kemp K., Johnson D.,
M. Kramer J., Filton L., Miller M., Creco T., Kemp K., Johnson D.,
M. Malson J., Spieth J., Payan B., Andrews S., Colson M., Joshu C.,
Antonolus B., Zidanid M., Strong C., Sun H., Lamax B., Yordan C.,
Antonolus B., Zidanid M., Strong C., Sun H., Lamax B., Yordan C.,
M. M. P., Zibney J., Preston K., Vill D., Slekher M., Matero A., Shah R.,
Swaby I. X., O'Shaughmessy A., Rodriguez M., Hoffman J., Till S.,
M. Granat S., Shohdy M., Hasegawa A., Hodriguez M., Hodmson A.,
Chen B., Marta M., Mattensen R., Homed A., Lodhi M., Johnson A.,
M. Geaquence and analysis of Chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                  75 LDHQLKMHDLNTDQENLVGT -- HDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRTPCN- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 -----AGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 HXKSVRAMTLHPKENAFASASAD------NTKKFSLPKGEFCHNMLS---Q 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 FALSCHDNTVCSVFTRP-----TDPQVVTGSHDTTIKFWDLR----YGKTMSTLTH 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QTRCIRAF----PNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFK----CHRLKENNIEQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 IYPVNAISPHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHR--YPTSIASLA-----PS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 KIINAMAV-NEDGVMVTGGDNGSIWFWDWKSGHSFQQSETIVQPGSLESEAGIXAACYD 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 ISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDCAFYD-PTHAWSGG 74
                                                                                                                                                                                        NHELINE 402:78-777(159); WINDELSON OF PRI AND PRZA PHOSPHATASES.
-1- FUNCTION: PLEADOTROPIC REGULATOR OF PRI AND PRZA PHOSPHATASES.
-1- SINILARIY: CONTENT ON PREPARED FAMILY OF WID-REPRAT POTEINS.
-1- SINILARIY: BELGANGS TO THE PRILIFELE FAMILY OF WID-REPRAT POTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1, Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 175.5; DB 1; Length 4; Pred. No. 1.2e-07; 63; Mismatches 124; Indels
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                                                                                                                                                                                                                                                                                                                                                           433 463 N
486 AA; S4009 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SIMILARITY: Contains 7 ND repeats.
-:- SIMILARITY: STRONG, TO KO4G11.4 AND C1481.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 GGLDHQLKMHDLNTDQ-ENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRT---- 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 KTLVDTDHAPVTFVCFSPNGKYLLSAQLDSSLKLWD-----PKKAKPLKYNGHKNK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 GISSUKFSPNTSQFLLVSSWDTSVRLYDVPANS-MRLKYQHTGAVLDCAFYDPTHAW--S 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 25.6%; Pred, No. 21e-07; Sonse 173; DB 1; Length 501; Sensiarity 25.6%; Pred, No. 21e-07; Conservative 41; Mismatches 108; Indels 52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
13g-FEB-2008 (Rel. 41, Last amonotation update)
17g-FEB-2008 (Rel. 41, Last amonotation updathing protein 20302.2 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kelley P.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB22116996F85988 CRC64;
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ThreeTeo, Irmoniseo, whoo, ..

Pendon, Prodonoin, by Modo, ..

Prodon, Prodonoin, by Modo, 2, ..

PROSTIE, PROGOSTO, MOGO, 7.

PROSTIE, PROGOSTO, WO, PROSTIE, PROGOSTO, PROSTIE, PROGOSTO, WO, PROSTIE; PROGOSTO, WO, PROGOSTO, PROPERT, MO, PROPALL, WO, PROGOSTO, PROGOSTO,
286 NDGTTLAIASS----YMYEMDDTEHPE 308
                                                                                                          445 NTGSRLVTCEADKTIKMWKEDENATPE 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 AA; 54473 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 273978; CAA98293.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; T27513; T27513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome V.
                                                                                                                                                                                                                                                                                                                                                                                              YH92 CAEEL
Q23256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                  YH92_CAEEL
                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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182 TRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIY 235	KYCLFANMSVPLGKHIISGSEDGRILVWSIQTKQIVQILEGH 468	236 PVNAISFHNIHNTFATGGSDGFVNIW 261	469 TTPVLATOSHPTLNIIASGGLEPDNVIRIW 498	
182	427	236	465	
λŏ	QQ	ò	ପ୍ର	

Scarch completed: November 12, 2003, 20:09:20 Job time : 20 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

November 12, 2003, 20:06:37; Search time 41 Seconds (without alignments) 20:06:421 Million cell updates/sec

1772 1 MTGSNEFKLNQPPEDGISSV......DGIFIRQVTDAETKPKSPCT 328 US-10-084-700-2 Perfect score: Sequence:

ritle:

830525 segs, 258052604 residues Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

830525

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_archea:*
sp_bacteria:*
sp_tungi:*
sp_tungi:*
sp_tungi:*
sp_invertebrate:*
sp_mamal:*
sp_mamal:*
sp_organelle:*
sp_plant:* SPIREMBL 23:* 10: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. sp_rvirus:* sp_bacteriap:* sp_archeap:*

					SUMMARIES	
Result		* Query				
No.	Score	Match	Match Length DB	DB	1D	Description
1	1651	93.2	324	13	098UH2	Oggisho wendered
~	1651	93.2	330	13	09YGY3	Ogvav3 xenonis lae
m	1050,5	59.3	326	ń	OSVAJZ	Ogvai2 drosophila
4	1035.5	58.4	326	'n	O9XXF7	Obruf J drosophila
2	949	53.6	327	S	076523	
9	949	53.6	339	70	09C701	09c701 arabidonsis
7	939	53.0	340	10	9NPT60	Ogling arabidonese
80	822.5	46.4	323	S	OBMSW6	Osmeruf drosonbilla
6	710	40.1	343	'n	OHMX60	Ogywho Geonorhebdi
10	691	39.0	250	10	09C6C4	Ografic arabidopsis
11	671,5	37.9	357	m	059902	OS9902 emericalla
12	586	33.1	344	10	OBRYMI	Osrumi Orvza gatite
13	578.5	32.6	349	50	09SAJ0	Obsaid arabidonsis
14	541.5	30.6	362	٣	074224	074224 emericella
15	530.5	29.9	349	٣	O9HEB3	Osbeh2 neurospors
16	523.5	29.5	349	s	Q9GRX8	O9drx8 chironomus

Q9w2e7 drosophila	O42860 schizosacch	O8c570 mus musculu	Oscbu3 mus musculu	O8mpf0 taenia soli	O8la29 arabidoosis	Q9c795 arabidopsis	Ogcsi6 mus musculu	O9w1t0 drosophila		OBsrm6 encephalito	Q25349 leishmania	O8bh42 mus musculu	O8vz23 anabaena sp		arabidop	Osbhdl mus musculu	O9w3il drosophila	O82020 anabaena sp	OSCYOS mus musculu	OBizx3 mus musculu	O8kb12 chlorobium	O8v109 anabaena sp		schizosacc		рошо	homo	homo
Q9W2E7	042860	08C570	Q8CBU3	Q8MPP0	08LA29	09C795	918260	Q9W1T0	Q8T4A6	QBSRM6	025349	Q8BH42	Q8YZ23	O820R1	09LM00	QBBHD1	Q9W3J1	082020	69CX09	Q8JZX3	Q8KB12	Q8YL09	QBYMU3	09C1X0	095320	QBNBTO	Q8N136	Q8N776
S	m	7	11	S	10	9	11	'n	s	ഗ	ß	1	18	16	10	7	Ŋ	16	።	11	16	16	16	m	4	4	4	4
346	320	368	341	208	314	315	82	336	336	318	339	45	934	1227	140	476	358	1747	356	405	329	1189	1551	297	357	407	415	415
29.4	29.3	29.5	28.7	27.8	25.8	25.5	24.3	18.3	18.3	17,8	15.3	13.0	12.1	11.6	11.2	11.2	11.1	11.0	10.8	10.8	10.6	10.6	10.6	10.5	10.5	10.5	10.4	10.4
521.5	518.5	517	208	492	457	452.5	431	325	325	316	272	231	215	206	198.5	198	196	194.5	192	192	188	187	187	186	185.5	185.5	184.5	183.5
17	18	19	20	53	22	53	24	52	56	27	28	53	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African claved frog).
Bukaryota Netazoa, Chordata, Cranlata, Vertebrata; Buteleostomi,
Amphibas, Barredhas Amura, Mesobarredha; Pipoides, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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93.2%; Score 1651; DB 13; Length 324;
Best Local Similarity 93.2%; Pred. No. 2.8e.193;
Matches 302; Conservative 14; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATT. 1801. 11:141-150(2001).

PRESIZE THOSE OF THE SECOND SECOND
                                                                                                                                                                                                                                                          0:-UW-2001 (TrameLrel. 17, Created)
01-UW-2001 (TrameLrel. 17, Last sequence update)
01-OUT-2002 (TrameLrel. 22, Last annotation update)
WD repeat protein Bub3.
                                                                                                                                                 324 AA.
                                                                                                                                       PRT;
                                                                                                                                       PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maturation.";
                                                                                                                             098UH2
RESULT 1
Q98UH2
                                                                                                                                                                                                      PAC OCC CON DATA SERVING CON DATA SERVIN
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1 MTGSNEFKLNQPPEDGISSVKFSPNTSQPLLVSSWDTSVRLXDVPANSMRLKXQHTGAUL 60

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                                                      241 SFHWIHWTFATGGSDGFVNIWDPPWKKRLCQFHRYPTSIASLAFSWDGTTLAIASSYMYE 300
187 QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSLEVQKKKYAFKCHRLKENNIEQIYPVNAV 246
                                                                                247 SPHNLHNIFAIGGSDGFVNIMDPENKKRLCQFHRYPISIASLAFSNDGSTLAIAASYMYE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BUBD spretein.
BUBD OR (CTSA).
BUBD OR (CTSA).
BURDOPALS Handpaster (Fruit fly).
BURDOPERS, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota, PRADERT, METAZOA, Diptera; Metachycera; Muscomorpha, Ephydroidae, Drosophilidae, Brosophilia.
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annocation update)
                                                                                                                                                                                                                                                                                                                                                     326 AA.
                                                                                                                                                                    301 MDDTEHPEDGIFIRQVTDAETKPK 324
                                                                                                                                                                                                  307 MDDIDHPEDALYIROVIDAETKPK 330
                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00320; WD40; 5.
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FlyBase, FBgn0025457, Bub3.
InterPro, IPR001680, WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00400; WD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                   Q9VAJ2;
                                                                                                                                                                                                                                                                                                                                                          Q9VAJ2
                                                                                                                                                                                                                                                                                                   RESULT 3
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                                                                                                                                                                                                                                                                                                           61 DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVBYCPEVNVMVTGSWDQTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 DCAFYDPTHAWSGGLDHQLKMHDIANTDGDTVVGSHDAPIRCYEYCPEVNVIVTGSWDQTV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQ1YPVNAI 240
                                                               DCAFYDPTHAMSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
                                                                                            61 DCAFYDFTHAMSGGLDHQLKWHDLNTDGDTVVGSHDAPIRCVEYCPEVNVIVTGSMDQTV 120
                                                                                                                                                                        121 KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY 180
                                                                                                                                                                                                      181 OTRCIRAPPNKOGVULSSIEGRVAVEYLDPSPEVOKKKYAFKCHRLKENNIEQIYPVNAI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 MTGSNEFKLNQAPEDGISAVKPSPNTSQFLLVSSWDSSVRLYDVPANTMRLKYQHAGPVL 66
            1 MTGSNEPKLNQAPEDGISAVKFSPNTSQFLLVSSWDSSVRLYDVPANTMRLKYQHAGPVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MTGSNEFKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A cact T. Kineshia T. Attendance of Microsine and Microsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
10-CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.2%; Score 1651; DB 13; 93.2%; Pred. No. 2.9e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 302; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 MUDITEHPEDGIFIRQVIDAETKPK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 MDDIDHPEDAIYIRQVIDAETKPK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99196240; PubMed=10098604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae, Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitotic checkpoint.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09YGY3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9YGY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
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66 DPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWPP 125
                                                                65 DIVHVVSGSLDNQLRLFDVNTQAESTIGAHEEPIKCLEHAEYVNGILTGSWDNTVKLWDM 124
                                                                                                                                                                                                                                                                                                                                                                                                     185 IRLFPWKEGYWASIEGRVAVEYLDHDFEVQRRKFAFKCHRNREQNIEQIYPVNALSFHN 244
                                                                                                                                                                                     126 RTPCNAGTFSQPE-KVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRC 184
                                                                                                                                                                                                                                                                                                                                                        185 IRAFPUKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISFHN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 IHNTFATGGSDGFVNIWDPFNKKRLCOPHRYPTSIASLAFSNDGTTLAIASSYMYEMDDT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 DPTHANSGGLDHQLKWHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 EFKLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVLDCAFY 65
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MEDILISE-19115384; PubMed-9914369;
MEDILISE-19115384; PubMed-9914369;
MEDILISE-19115384; PubMed-9914369;
MEDILISE-19115384; PubMed-1914369;
MEDILISE-19115384; PubMed-1914369; Bouchard N.L.;
MEDILISE-191454; PubMed-191454; PubMed-1914544; PubMed-191454; PubMed-191454; PubMed-191454; PubMed-191454; PubMed-191454; PubMed-191454; PubMed-191454; PubMed-191454; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

WAS ALL LOGARISHO, E., Herrman S., Bousbaa H., Li Z., Chan G.K.T.,
Yen I.J., Schald C.E., Goldberg M.L.,
Yen I.J., Schald C.E.,
Yen S. H. S., Schald C.E.,
Yen S. H. S., Schald C.E.,
Yen S. H. S., Charles S. H. S., Schald C.E.,
Chicacocome cequires Bubl but not ZwiO or Rod.";
Chicacocome of 0.0-011998]
                                                                                                                                                                                                                                   8; Gaps
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Drosophila melanogaster (Fruit fly).

Medroyte, Netzaza, Arthropoda; Nedapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Nedirakches; Prosophilidae; Drosophila.

Nedirakcher277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Owery Match 53.64; Score 949; DB 5; Length 327; Befer Local Similarity 56.38; Pred. No. 1.5e-76. Medls Matches 183; Conservative 50; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mitotic checkpoint control protein BUB3.
BUB3 OR GG7881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 IRLPPNKEGYVMSSIEGRVAVEYLDHDPEVQRRKFAFKCHRNREQNIEQIYPVNALSFHN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 RTPCNAGTFSOPE-KVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRC 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                            Query Match 59.34; Score 1050.5; DB 5; Length 326; Rest Local Similarity 60.45; Pred. No. 130-85; Masches 195; Conservative 49; Mismatches 75; Indels 3;
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Makyyten, Westanoa, Arthropdan Hekapoda, Insecta; Pterygota, Neoptera; Endopteryota, Diptera, Endoptery, Endopteryota, Diptera, Etahycera; Muscomorpha, Negl'arkin-7277;
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A drosophila homolog of Bubla.";

Publicate Fargonostaty To the EMEL/CenBank/DoBJ darabases.

EMEL, AFJOGST9, AAD21971.1;

Threarbo, IRROGSG9, MA01.9 in the Press of P
01-4007-1999 (TREMBLEL] 12, Created)
01-4007-1999 (TREMBLEL] 12, Last sequence update)
WD-40 repeat protein. 22, Last amnotation update)
WD-40 repeat protein.
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Matches
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129 ASGTERTQIGTYMQPERVNSISLVGNRLVVATAGRHVNIYDLRNMSQPEQRRESSLKYQT

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68 THAMSGGLDHQLKWHDLMTDQEMLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRT

10 ELSNPPSDGISNLRFS-NNSDHLLVSSWDKSVRLYDANGDLMRGEFKHGGAVLDCCFHDD 68

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TREATMENT COLUMBIA:

KEDLATHER, COLUMBIA:

THEOLOGIS A. ECKET JR. Palm C.J., Federspiel N.A., Kaul S.,

NATION COLUMBIA:

THEOLOGIS A. ALEAGUA PARADIO R., BOOMBAD C.L., BEDOKS S.Y.,

NATION C.A. Alonso D. A. Aleaf H. A. Arajo R., Chenk, C. Chin C.,

A. Chung M.K., Cohn L., Conway A.B., Chesay T.H., Dewar K.,

A. Chung M.K., Cohn L., Conway A.B., Chesay T.H., Dewar K.,

A. Minner J.E., Goldemich A.D., Rasa B., Mansen N.F., Hughes B., Maizer M.

A. Manner J.E., Goldemich A.D., Rasa B., Mansen N.F., Manses B., Manser J.L.,

A. Minner J.E., Coldemich A.D., Rasa B., Mansen N.F., Manser B.,

A. Minner J.E., Manner B., M. L., Ludove S., Mait H., A. Manser B.,

A. Milliecher J., Mittanda M., Mayure M., Nierman N.C., Goberne B.,

A. Sakano L., Salaerg S.L., Schwartz J.R., Shinn P., Southwick P.,

A. Sakano L.J., Trabhagung G., Torium M.J., Town C.D.,

A. Manner, Tallon L.J., Trabhagung G., Torium M.J., Town C.D.,

A. Manner, T., Wan Aken S., Waysberg W., Wydocskala V.S., Walker M.,

M. D., Yu G., Fraser C.M., Wenber J.C., Balak R.,

Y. Seagenone, and analysis of chromosome 1 of the plant Araidopsis
65 DIVHVVSGSLDNQLRLFDVNTQARSIIGAHERPIRCVSHARYVNGILIGSWDNTVKLMDM 124
                                                               126 RTPCNAGTFSQPE-KVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRC 184
                                                                                               185 IRAF---PNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAIS 241
                                                                                                                                                                                   242 FHNIHNTFATGGSDGFVNIWDPFNKKRLCOFHRYPTSIASLAFSNDGTTLAIASSYMYEM 301
                                                                                                                                                                                                                                                                    243 FHNVYQTFATGGSDGIVNIWDGFNKKRLCQFHEYDTSISTLNFSSDGSALAIGCSYLDQL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryotai Viridiplantae, Streptophyra; Bmbryophyta; Tracheophyta;
germatophyta; Wagnoliophyta; eudicoryledons; oore eudicots; Rosidae;
eurosida [1] Brassicales; Brassicacees, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATIVE: PROMOJO: CREATERINBRP.
SMART: SHOOTOO, WHO! S. TAN EXPERTS 2. 2.
REGETTE: PESSORS! WD. REVERTS 2. 2.
REGETTE: PESSORS! WD. REVERTS. REGTON; 1.
REPER: MD. REPER. 37570 MM; 738570 MM; 738570 MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CTR-2002 (TrEMBLrel. 22, Last annocation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 339 AA.
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Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                    302 DDTEH- - PEDGIFIRQVTDAETKPK 324
                                                                                                                                                                                                                                                                                                                                                                          303 PETPATVPHPAIYÍRYPTDQSTKQK 327
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BMBL, ACO4410, AAG6165-1; -.
InterPro, IPR001680; WD40.
Ffam: PF00400; WD40; S.
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Nukamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl.
TAC and BAC clones."
                                                                                                                                                                      Eukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Residentes, Streptophyta, Sagnoliophyta, endicotyledons, core eudicots, Rosidae, auroside II; Brassicales, Brassicaceae, Arabidopeis, Noni-Taxibaji02,
                                                                                                                                                                                                                                                                                                        STRIN-Columbia;
Ranko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitred (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

BERGAR B.L., "DOWN C.D., Troukhan M., Alexandrov N. Peldmann K.A., Flavell R.B., White O., Salzberg S.L.;

Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;

*Pull-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Secore V., Lu Y.-P., Plavell R., Feldmann K.; Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "MAIL-GREACH CONK FOR ARRAIGODS; a thallana.";
Submitted (NMS-2002) to the EMEL/GenBank/DDEJ databases.
EMEL ANDONIAT. BENEZOSTA: 11. "
Theorem 178001540; ANG4953.1; "
Theorem 178001540; NUO.
FRAME. PRODOIS OF THE PROPERTY PRODOIS OF THE PROPERTY PRODIS OF THE PROPERTY PRODIS OF THE PROPERTY PRODIS OF THE PROPERTY PRODIS PRODIS OF THE PROPERTY PRODIES.
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                                                                           01-007-2000 (TERMELCE] 15, Created)
01-007-2000 (TERMELCE] 15, Last sequence update)
01-007-2000 (TERMELCE] 21, Last amouation update)
Mitoric checkgonin protein putairo, mutaivo
Arabidopsis thaliana (Mouse-ear creas).
                                       340 AA.
                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 7:217-221(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        annotation.";
Genome Biol. 0:0-0(2002).
                                       PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; WD repeat.
SEQUENCE 340 AA;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Columbia;
                                                             OPLINB;
                                       90LJ90
RESULT 7
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8 KLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVLDCAFYDP

6; Gaps

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65 DIVHVVSGSLDNQLRLFOVNTQAESIIGAHEEPIRCVEHAEYVNGILTGSWDNTVKLWDM 124
66 DPTHAMSGGLDHQLKNHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AL032648; CAA21698.1; -. WormPep; Y54G9A.6; CE19233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 12,
(TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                       245 IHNTFAT 251
                                                                                                                                                                                                                                                                                                                                                        245 UYQTFAT 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y54G9A.6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01#MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y54G9A.6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9XWH0
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
Q9XWH0
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                                                                                                                                                                                                                                  176 SSLKYQTRCIRAFPNKQGXVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                         183 SSLKYOTRCVRCYPNGTGYALSSVEGRVAMEFFPLSEAAQAKKYAFKCHRKSEAGRDIVY 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 PWNAISFHNIHWFFATGGSDGPVNIMDPPNKKRLQPHRYPTSIASLAFSNDGTTLAIAS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVCTHDAPIRCVEYCPSVNVMVTGSWDQTV 120
                                                                                                                                                                                                                                                                                                       121 KLWDPR-----TPCNAGTPSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRE 175
                                                                                                     9
                                                                                                                                 4 VTPSAGRELSNPPSDGISNLRFS-NNSDHLLVSSWDKRVRLYDVSTNSLKGEFLHGGAVL 62
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                                                                                                     1 MTGSNEFKLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                    6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Clampe W., Chavez C., Dorsett V. Dresenk D. Farten D. Frise E., George R., Gonzalez M., Gaarfin H., Krommiller B., Lis P., Liso G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Man K., Yu C., Lewis S.B., Ribin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Bikaryotes Medaroda Athibogoda Hakarpoda Insecta; Fterygota;
Meoptera; Endopterygota; Oppera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.4%; Score 822.5; DB 5; Length 323; 60.7%; Pred. No. 3e-65;
Query Match

23.0%; Score 939; DB 10; Length 340; Betriocal Similarity 54.1%; Pred. No. 1.3e-75; Matches 178; Conservative 54; Mismatches 91; Indels (Matches 178; Conservative 54; Mismatches 91; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40, Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sponitred (UNY-2002) to the EMBL/GenBank/DDEJ databases. 
EMBL, ATIRSSS, TAMA99895.1; - 
FLYBess; FEGNOSS457; BND. 
InterPort | EMOUSES, WARD. 
FRAME, PRODAGO, WIGH. 
PRIMES, PRODAGO, WIGH. 
SMRZT, SMOSSOJ WHOU; A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 SYMYEMDDTEHPEDGIFIROVTDAETKPK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 SYTFEEGEKSQEPEAIFVRSVNEIEVRFK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS00678; WD REPEATS 1; 1.
PROSITE; PS50082; WD_REPEATS_2; 1.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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61 DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
126 RIPCNAGIFSQPE-KVYILSVSGDRLIVGTAGRRULVWDLRNMGYVQQRRESSLKYQTRC 184
                                              125 REKRCVGTFBONNGKVYSMSVIDEKIVVATSDRKVLIMDLRKMDSYIMKRESSLKYOTRC 184
                                                                                                               185 IRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVWAISFHN 244
                                                                                                                                          121 KLWDPRTPCNAG--TFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 KYQTRCIRAFPUKQGYVLSSIBGRVAVEYLDPS-PEVQKKKYAFKCHRLKE-NNIEQIYP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 NEFKLNOPPEDGISSVKFSPNT-SQFLLVSSWDTSVRLYDVPA---NSMRLKYQHTGAVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 NEFRVFFPFVQISKVQFQREAGSRLLAASGWDGTCRVYEVGKLGDISEKLVFTHGKPLL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans: A platform for investigating biology,"; Science 282:2012-2018(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.6%; Pred. NO. 3.7e-5-,
tive 67; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS: PROGAZO, CROPERINBRY.
PROGATES: PROGAZO, MULO, 3.
PROCATE: PSOGAC'8; NO. REPERING_21, 1.
PROCATE: PSOGAC'8; NO. REPERING_22, 2.
RECATE; PSOGAS; NO. REPERING_RECAIN; 1.
REPERING_ATS: PSOGAS; NO. REPERING_RECAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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55 HTGAVIDCAF-YDPTHAMSGGLDHQIKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 HRAPVLDACFGATEDEIFTAGLDWDVKRIDIASASGTVLSSHDAGVRSVVYSKEYSWVIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 ASWDWTLHVHRLAGDRSVTWTASIPLPSKPFSMSLTATKLVVGMASRALHIYDLKSLSLL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .14 GSWDQTV---KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 Q------QRRESSLKYQTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 TGQSEGGVAPAKVEVEPWQRRESSLKFMTRCVACMPDDAGYASSSIEGRVAVEWFDPSAE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 VQKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNTPATGGSDGFVNIMDPFNKKRLCQFH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 SOARKYAFKCHROTSDDVDVVYPVNSLAFBPHGTFASGGGDGVVALWDGIAKRRIROYO 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SNEFKINOPPEDGISSVKFS--PNTSQFLLVSSWDTSVRLYDV-----PANSMRL--KYQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SNOFTITSPPTDAISALKFSPAPDSTRF-VVSSWDKNVYVYDLRDENGAAGEGKLLOKFE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A screen for dynain synthetic lethals in Aspergillus nidulans didentaties againtle assembly checkpoint genes and other genes involved in detrosts.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.9%; Score 671.5; DB 3; Length 357;
39.2%; Pred. No. 1.1e-51;
Live 79; Mismatches 101; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 RYPTSIASLAFSNDGTTLAIASSYMYEMDDTEHPEDG---IFIRQVTDAETKPK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bmericella nidulans (Aspergillus nidulans).
Enkaryota, Pungi, Ascomycota, Pesisonycotina, Eurotionycetes;
Eurotaisles, Trichocomaceae, Emericella.
NEB. Taxabai63425,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNAPT, SKONOJO, NEDGI, 4.
PROGITE, PSSOGJS4, ND_REPERIS_2, 2.
PROGITE, PSSOGJS4, ND_REPERIS_REGION; 2.
REPERI, ND_TEPERIS_C.
SEQUENCE TO STO AAJ, SURJAM, B072A809CA3FSE6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TrEMBire). 07, last sequence update)
01-AMR-2003 (TrEMBire). 23, last annotation update)
Spinide assembly checkpoint protein 51DB.
                                                                                                                                                                                                                                                                                                                                                357 AA.
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01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                          PRT;
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EMBL; AR032988.1; -.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 39.3%
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                          243 H 243
                                                                                                                                                                                249 H 249
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          237 VAAISFHAIHNTRATGGSDGFVAIMPPRIKRILCÇFRRYPTSIASLAFSNOGTILAIASS 296
285 VHTVARIPKITGFRATGGAGAIWIMPPRIKRIIQLIRFEFTSISSLSREDGGQLAATS 313
285 VHTVARIPKITGRATGAAGAIWIMPPRIKRIIQLIRFEFTSISSLSREDGGGLAATS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 THAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVNVTGSWDQTVKLWDPRT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 SSGFSVCADTKVRRIDENAGKEDVLGTHERPVRCVEYSYAAGQVITGSWDKTIKCWDPRG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 PCNA----GTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 RCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISF 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ELSNPPSDGISNLRFS-NNSDHILLVSSWDKSVRLYDANGDLWRGEFKHGGAVLDCCFHDD 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Viridiplantae; Streptophyra; Embryophyra; Tracheophyra; Spermateophyra; Tracheophyra; Spermateophyra; Magnollophyra; Magnollophyra; audiocyledons; coxe eudicocs; Rosidae; entosida II; Baxasicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                01.-UNN-2001 (TrEMBLrel. 17, Greated)
01.-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01.-UN-2002 (TrEMBLrel. 22, Last annotation update)
01.-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitotic checkpoint protein, 3' partial (Pragment)
                                                                                                                                                                                                                                                                                                                                                                                250 AA.
                                                                                                                                                297 YMY - - EMDDTEHPEDGIFIROVTDAETKPK 324
                                                                                                                                                                                          Nature 408:816-820(2000).
BMEL, ACOPS64:1, AAG31772.11.
TITESPEO, TERRO1680; MP40.
PRAMIT, SMO320; MP40. 4.
PROSTET, BROSOSS, MP40. 4.
PROSTET, BROSOSS, MP40. 4.
REPRET, MP40. 4.
REPRETAR 
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116 WDQTVKLWDPRTPcNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRE 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 SPLKYQTRCVTAPPDQQQFLVGSIEGRVGVHHLDDSQ--QSKNFTFKCHR--DGN--DIY 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 NKSYEVTPSPADSISSISFSPR-ADILVATSWDNQVRCWEISRSGASLASAPKASISHDQ 73
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Gonsalez A., Liu A., Liu K., Sasano H., Koor T., Pham P., Vayaberg M., Newg B., Chin C., Choi E., Chinu J., Allafi H., Brooks S., Chao O., Corneay A., Harsen M., Johnson-Hopson C., Khan S., Kin C., Lam B., Mayvar M., Palm C., Shinn P., Tambunga G., Bavis R.M., Theologis A. Theologis S., The C., Shinn P., Tambunga G., Bavis R.M., Theologis A. H., Sederspiel M.A., Theologis A.; Sasanda A. Davis S., Shinn M. Shinn 
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Haas B.J., Volforsky N., Town C.D., Troukhan M., Alexandrov N.,
Fadidman K.A., Flavell R.B., White O., Salzberg S.L.,
Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eriover V., Troukhan M., Alexandrov N., Lu Y.-P., Flawell R., Feldmann K.; Proll-length conk from Arabidopsis thalians "; Submitted (MAR-2002) to the RWIL/GenBank/DDBJ databases. PRBL, Acol1713, ARAF6251, ". PRBL, ACOL1713, ARAF6250, 1, ".
                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 349 AA; 38268 MW; F1780EF3258C5632 CRC64;
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(TrEMBLrel, 08, Last sequence update)
(TrEMBLrel, 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro. IPROULES(N. WD40.)
Fram. PF00400, WD40. 5.
PRINTS; PROUSZO; GRROTEITBRRPT.
PROITE; PSSO082, NO. REPERTS. 2; 4.
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                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVKLWDPRTPCNAGTPSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 KYQTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKYAFKCHRLKENNIEQIYPVN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 AISFHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYM 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 ALNFHPVHHTFATSGSDGGFNFWDKDSKQRLKAFNKCPSPITCSTFNQDGSIFAXAVCYD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 SNEFKLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDV-PANSMRLK--YQHTGAVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bikaryota, Viridiplantae; Streptophyra; Embryophyra; Tracheophyra;
Spermatophyra, Magnoliophyra, eudicotyledons; core eudicots; Rosidae;
eurosida II; Brassicales; Brassicaeae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. COlumbia,
Schwartz S.R., Yu G. Toriumi M., Lenz C., Liu S., Lee.J.M., Li J.,
                                                                                                                                        Obyza sativa (japonića cultivat-group)
Opyza sativa (japonića cultivat-group)
Sprancopolyca (Magnoliophyta; Liliopsida; Poales; Poaceae;
Espancopoliophyta; Oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. Nipponbare; Sasaki T., Watsuncto K.; Matsuncto T., Yamamoto K.; Oryza sastiva nipponbare(GA3) genomic DNA, chromosome 1, PAC clone: 9065310. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.1%; Score 586; DB 10; Length 344; 38.8%; Pred, No. 4.5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 128; Conservative 68; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 AA; 37849 MW; 9C6690219F6001EC CRC64;
     01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Putcative mRNA export protein.
P0663E10.24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2(form2) (mRNA export protein, putative)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 YEMDDTEH----PEDGIFIRQVTDAETKPK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 WSKGAEKHNPSTAKTNIFLHSVQESEVKGK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00400; MD40; 4.
SMART; SM00320; WD40; 5.
SMOSITE; PS50082; WD REPEATS 2; 4.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP004317; BAB90741.1; -. Gramene; Q8RYM1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; WD repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=3702;
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62 CAFYDPTHAWSGGLDHQLKWHDLNTDQENLVGTHDAPIRCVEYCPEVN --- VMVTGSWDQ 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 TVKLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSL 178
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                                                                                                                                                                                                                                                                                                                                                                            6 EFKINQPPEDGISSVKFSPNTS---QFLLVSSWDTSVRLYDVPANSMRLKYQHTG-AVLD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                         22 DVELGQPPEDSISDLAFNPNPADQKDFLAVASWDKKTRIYBILSNG-----QGQGQAMIR 76
                                                                                                                                                                                                                                                                                                               21; Gaps
                                                                                                                                                                                                                                             Query Match

29.9%; Score 530.5; DB 3; Length 349;
Beef Local Similarity 37.5%; Pred. No. 4.2e-39;
Bect Local Similarity 54; Mismatches 123; Indels 21;
                                                                                                                                                  Repeat, WD repeat.
SEQUENCE 349 AA; 38197 MW; E42D4C739B2430D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 ----MYEMDDIEHPEDGIFIROVTDAETKPK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 DWSKGYQGNSPTYPTK-VMLHPVQQDECKPR 343
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                         Pfam, PF00400; WD40; 5.
MART, SW00320; WD40; 3.
PROSITE; PS50082; WD REPEATS 2; 2.
PROSITE; PS50294; WD_REPEATS_REGION; 2.
InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 GSWDQTVKLWDPRIPCNAGIFSQPEKVYILSVSGDRLIVGTAGRRVLVWDLRNMGYVQQR 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 GSWDKQVKYWDLRQSTPIASLECQERVYTWDVKDKLLVIGTADRYINIVDLANPTKFYKT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 RESSLKYQTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPBVQKKKYAFKCHR---LKENN 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 IBQIYPVNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 INNIXSVNAISFHPVHGTESTAGADGTFHFWDKDAKHRLKGYPSVGGTISSTAFNRTGNI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SNEFKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSM---RLKYQHTGAVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 SKDVALNSPPEDSISDLRFSP-ASEHLAVASWDKKVRIYEINEQGQSEGKALFEHEAPVL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCHDILLE U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Wakaturs G., Heves H. H., Mannhaupt G., Submitted (DEC. 2000) to the BMEL/Gengank/DDBJ detabases.
                    Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotialas; Trichocomaceae; Emericella.
NOBI—Taxib=16245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.6; Score 541.5; DB 3; Length 362; Best Local Similarity 36.24; Pred. No. 46-40; Merches 122; Conservative 53; Mismatches 143; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
Mararyota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariacese; Neurospora.
                                                                                                                                                                                                               German Neurospora genome project;
submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL431109; CAC18615.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AA; 39697 MW; 1E2BA0BFBFFD101E CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 LAIASSYMYEMD---DTEMPEDGIFIRQVTDAETKPK 324
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Emericella nidulans (Aspergillus nidulans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS50082, WD REPEATS 2, 2, PROSITE, PS50294, WD_REPEATS_REGION; 1. Repeat, WD repeat.
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01-WAR-2001 (TrEMBLrel. 16, Last sequ
01-WAR-2003 (TrEMBLrel. 23, Last anno
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                                                                                                                                                                                           MEDLINE=98311642; PubMed=9647650;
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                                                                                                                                                       SEQUENCE FROM N.A.
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OM protein - protein search, using sw model

Run on:

November 12, 2003, 20:07:13 ; Search time 20 Seconds (Without alignments) 1577,166 Million cell updates/sec

1 MTGSNEFKLNQPPEDGISSV..........DGIFIRQVTDAETKPKSPCT 328 US-10-084-700-2 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283308 segs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: Dirl:*
2: Dir2:*
3: Dir3:*
4: Dir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ķ				
Result		Query				
No.	Score	Match	Match Length	20	ę,	Description
1	93	53.0	340	~	T52386	mitotic checkpoint
CV	710	40.3	343	ď	T27185	hypothetical prote
m	578.5	32.6	349	~	A96839	F23A5.2(form2) [im
4	538	30.4	365	C	850610	건
2	518.5	29.3	320	N	T38301	probable mitotic c
9	511.5	28.9	352	N	A56119	RNA export protein
7	418.5	23.6	373	~	T20723	hypothetical prote
00	356	20.1	341	Н	339654	cell cycle arrest
Ø1	352.5	19.9	251	N	871241	probable RNA expor
10	272	15.3	339	٩	T02818	polyA export prote
11	228	12.9	1526	N	AC2239	repeat
12	215	12.1	934	N	AG1889	
13	209	11.8	1258	a	AI2155	WD-repeat protein
14	206	11.6	1227	N	AE1810	WD-40 repeat prote
15	198.5	11.2	140	N	H86292	F7H2.18 protein -
16	194.5	11.0	1747	N	AC1842	WD-40 repeat prote
17	187	10.6	1189	N	AI2493	WD-repeat protein
18	187	10.6	1551	C)	AB2410	WD-repeat protein
13	181	10.2	304	N	AG1837	WD-40 repeat prote
20	178.5	10.1	1189	ď	AH2154	WD-repeat protein
21	177.5	10.0	356	c	T22478	hypothetical prote
22	176.5	10.0	677	~	AE1861	serine/threonine k
23	176	6.6	1356	~	T18521	beta transducin-li
24	175.5	6.6	486	ď	\$49820	PRL1 protein - Ara
25	173	8.6	501	~	T27513	hypothetical prote
56	171.5	9.7	196	~	E86245	-
27	169.5	9.6	340	-	RGHUB1	
28	169.5	9.6	340	ч	RGBOB1	
29	169.5	9.6	340	N	JC5057	G protein beta 1 -

PRL2 protein - Ara	transcription init	WD-40 repeat regul	WD-40 repeat prote	CDC40 protein - ye	GTP-binding regula	hypothetical prote	hypothetical prote	WD-40 repeat regul	trp-asp repeat con	hypothetical prote	beta transducin-li	WD-40 repeat prote	GTP-binding protei	GTP-binding protei	GTP-binding regula
549821	T39490	T46032	AD1842	561159	511904	\$56893	AH2195	558306	T41148	AB2202	T42045	AF2071	T16987	T16970	T02340
~	6	N	N	~	2	~	~	a	N	~	~	~	N	a	2
431	642	317	1711	455	318	714	949	614	502	559	1049	1683	326	328	326
9.8	9.5	9.5	9.8	9,4	4.6	9.3	9.3	9.3	9.3	9.5	9.5	9.5	9.5	9.5	9.1
169	168.5	167.5	167.5	167	166	165.5	165	164.5	164	163.5	163.5	163.5	162.5	162.5	161.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	42

ALIGNMENTS

RSUUT 1 192386 Horto: Gheckpoint protein [imported] - Arabidopsis thaliana C.Species Arabidopsis thaliana (mouse-ear cress)

Kidareo, 1; ARCA II; Saco, 2; NaKamira, 1; samillu, E.; Tab unmittee, 0; Lie and Lie a

6; Gaps Ouery Match 53.0%; Score 939; DB 2; Length 340; Best Local Similarity 54.1%; Pred. No. 7.2e-73. Matches 178; Conservative 54; Mismatches 91; Indels Matches 178; Conservative 54; Mismatches 91; Indels

61 DCAFYDPTHAMSGGLDHQLKAHDLNYDQENLVGTHDAPIRCVEYCPEVNVMVTGSMDQTV 120 63 DCCFHDDFSGFSVGADYKVRRIVFNVGKEDILGTHDKAVRCVEYSYAAGQVITGSWDKTV 122 121 KLWDPR-----TPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNWGYVQQRRE 175 1 MTGSNEPKLNOPPEDGISSVKFSPNTSOFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL 60 g ò 셤 à g

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hypothetical protein Y54G9A,6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

A;Map position: 2 A;Introns: 78/3; 291/2 C;Superfamily: unassign

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Nayorbaking notesin YER107 - yeart (Saccharomyces cerevisiae)

(Species Saccharomyces cerevisiae
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Albertichion SMELU188399, NID3:RENI07c
Albertichion SMELU188399, NID3:RENI07c
Albertichion SMELU188399, ARD2-
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First-Scholmanit: WD repeat homology 4002-
First-Mobilis MD repeat homology 4002-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 SPLKYQTRCVTAFPDQQGFLVGSIEGRVGVHHLDDSQ--QSKNFTFKCHR--DGN--DIY 247
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38.7%; Pred. No. 6.5e-42;
iive 60; Mismatches 125; Indels 19; Gaps
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Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KIMDPRIPCNAG- - IFSQPEKVYILSVSGDRLIVGIAGRRVLVMDLRNMGYVQQRRESSL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 KYOTRCIRAFPNKOGYVLSSIEGRVAVEYLDPS-PEVOKKKYAFKCHRLKE-NNIEOIYP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 KYOTRAVOFFPTGEAFVVSSIEGRVAVEVVDOSGEEMMKRKYAFKCHREKDTDGTELIHP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237 VNAISPHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 VHIVAPHPKYGIFAIGGADGIVNIWDPPNRKRIIOLHKPEISISSLSFNEDGSOLAIAIS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 NEFKLNQPPEDGISSVKFSPNT-SQFLLVSSWDTSVRLYDVPA---NSMRLKYQHTGAVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 NEFRVPFPFVOISKVOFOREAGSRLLAASGWDGTCRVYEVGKLGDISEKLVFTHGKPLL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Wolecule type: DNA
A;Residuce: 1.549 <RD>
A;Cross=reference: GB:AB005173; NID:g6503279; PIDN:AAF14655.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79345.2(form2) (imported) - Arabidopsis thaliana
C.59ecesa Arabidopsis thaliana (mouse-aer cross)
C.fore: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
       C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
C.Accession: T27185
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Ouery Match

Ouery Match

Out 1.00-1.30-1.00

Out Local Similarity 43-64, Pred. No. 9.30-53,

Matches 144, Conservative 67, Mismatches 109, Indels 10, Gaps
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A./Map position:
.SiSuperfamally: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: unassigned WD repeat proceins; WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 YOYEKEIDPSPLPNNSITIRHITDPESRPK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 YMY -- EMDDIEHPEDGIFIRQVIDAETKPK 324
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A,Status: preliminary

Genetics;

A:Accession: A96839

C;Accession: A96839

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AisCatus; preliminary, translated from GB/ENBL/DDBJ
AiNOLeonie: 1950 DNA
AiROSEONIE: 1-352 WEBL: ALO21748; PIDN: CANAGSS.1; GSPDB: GN00067; SPDB: SPEC16A3.05c
AiROSEONIE SPECIAIN 972A: Cosmid Ci6A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 KFQTRSLACFIKGDGYAIGSVEGRCAIQNIDEKNASQ--NFSFRCHRNQAGNSADVYSVN 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AF-YDPTHAWSGGLDHQLKMHDLMTDQBNLVGTHDAPIRCVEYCPEVN----VMVTGSWDQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 NWSRDGTKVASGSVDKSAKVFDIQTGQNQQVAAHDDAVRCVRFVEAMGTSPILATGSWDK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 TVXLWDPRTPCNAGTFSQPEXVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 TLKYWOLRQSTPIATVSLPERVYAMDCVHPLLTVATAERNICVINLSEPTKIFKLANSPL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 KYQTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 AISPHNIHNTPATGGSDGFVNIHDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSY- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 DVEVAQPPEDSISDIAFSPQ-AEYLAASSHDSKVRIYEVQATGQSIGKALYEHQGPVLSV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 BEKINGPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSM---RLKYQHTGAVLDC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: Z80216, PIDN: CAB02280.1; GSPDB: GN00019; CESP: F10G8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TGSNEFKLNOPPEDGISSVKFSPNTSQ--FLLVSSWDISVRLYDV-PANSMRUKYOHT-- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 TONDDFLVDGAPEDTIQVIKFSPTPQDKPMLACGSWDGTIRVWMFNDANTFEGKAQQNIP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F1008.3 - Caenorhabditis elegans
C.) Decises Caenorhalts elegans
C.) Decises (Senorhabs) shaqtus evision 15-Oct-1999 #text_change 26-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.9%; Score 511.5; DB 2; Length 352; 34.8%; Pred. No. 3.7e-36; tive 58; Mismatches 142; Indels 15; Gaps
R.Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R. submitted to the ERBL Oata library, February 1998
A;Reference number: 721862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Introns: 24/3; 50/2
S.Stoperfamily: unassigned WD repeat proteins; WD repeat homology
F;70-105/0main: WD repeat homology <WD.>
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A;Moleorie type: DNA
Asesidues: 1.373 «Mil.»
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submitted to the EMBL Data Library, September 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 --- MYEMDDTEHPEDGIFIRQVTDAETKPK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 WSKGYTENNAQLP-NKIMLHPVPQDEIKPR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Experimental source: clone F10G8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 115; Conservative
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A;Introns: 36/3; 67/3; 345/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Reference number: 219315
A, Accession: T20723
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                                                                                                                                                 A, Accession: T39547
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Cinces 12-Oct-1395 Requence Evision 13-Oct-1395 #text_change 26-May-2000

Cincession: A56119 Fissed Chosh, A.; Whalen, W.; Fitzgerald, E.; Dhar, R.

Ribrown, J.A.; Bharsthi, A.; 4395 A.; Ghosh, A.; Whalen, W.; Fitzgerald, E.; Dhar, R.

J. Biol. Chimer 200, "All 7415, 1395 A. Shitzsachoranquess pombe rael gene causes defects in poly(la) A; Reference number; A65119, MUD195221400; PMD57708237
                                                                                                                                                                                                                                                                                                                                                                                                    Comparization description who respeat protein - fission yeast (Schizosaccharomyces pombe Comparization delationsaccharomyces pombe Comparization delationsaccharomyces pombe Comparization delations of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization of the comparization o
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A;Experimencal source: strain 972h-; cosmid c23H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 TFSQP-----EKVYTLSVSGDRLIVGTAGRRVLVMDLRNMGYVQQRRESSLKYQTRCI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 -- KODVEGODIGKKIPASSSRDNILVLGCSBRENLVYDIRNLKLPPORRPSSFKYMTRSV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 RAFPNKQGYVLSSIEGRVAVEYLDPSPBVQKKKYAFKCHRLKENNIEQIYPVNAISFHNI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 CCNQNFEGFVSSSIEGRISVEYINPSQEAQSKNFTFKCHRQIQKDYDIVYPVNDLKFHPI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 HNTPATGGSDGPVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYMYEMDDTE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 NGQSLVYPVNSIAFHPLYGTFVTAGGDGTFNFWDXNQRHRL.---KGYPTLQASIPVCSFN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 GGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRTPCNAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 EDGISSVKRSPNTSQFLLVSSWDTSVRLYDVPANSMRL-KYQHTGAVLDCAFYDPTHAMS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 KDGISSVIPSPSVKNELIAGCWDGSLLHYQISENPELLGKYDLSSPILSLEYTDEKTALV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Gaps
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A;Residnes: 1.352 <BR
A;Cross.references: GB:U14951; NID:g625093; PIDN:AAA86311.1; PID:g625094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA export protein rael - fission yeast (Schizosaccharomyces pombe)
N/Alternate names: poly(a) + rna export protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.3%; Score 518.5; DB 2; Length 320; Best Local Similarity 36.1%; Pred. No. 8.2e-37; Merches 115; Conservative 52; Mismatches 131; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 108/1
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                               286 NDGTTLAIASSYMY---EMDDTEHPEDGIFIRQVTDAETKPK 324
                                                                                                                                                                      321 RNGSVFAYALSYDWHQGHMGNRPDYPNVIRLHATTDEEVKEK 362
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                      RESULT 5
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ŝŝ	111 NVTGSNDQTVKLMPPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVNDLRNM 167	Qy 151 IVGTA	151 INGTAGRRULWADLRNAGYVQQRRESSLKYQTRCIRAPPNKQ-GYVLSSIEGRVAV 205
96		Db 164 IVGMN	164 IVGARNSQVQMFRLPLCEDDNGTIEESGLKXQIRDVALLPKRQGEGYACSSIDGRVAV 220
& &	168 GYVQQRRBSSLKYQTRQIBAFBNKQGYVLSSIEGRVAVZYLDSPEVQKKKYAFK 222 207 PTEVXDIBEAKEARISTSTER 254 207 PTEVXDIBEAKEARISTSTER 264	Qy 206 EYLDP 	206 EYLDPSPEVOKKYKPKHILKENNIEDTYPVMAISPHIHYTRATOSDENNIUDP 263 221 EFFDDQQDDYNSSKRPAFCHRINIKÖTNLAYPWSIEFSPRIKFLYTNGSDGIISCMIL 200
& g	223 CHILKEWILEOLYPVALSPHVIHVTFATOSBOGFVHTWOPFNKKRLCOFHRYPSIA 260 265 CHRAELVALVOGITAVNOJCHOPGKLVITASBOGRVSWIKLARTKLKTSPHPHELT 324 565 CHRAELVALVOGITAVNOJCHOPGKLVITASBOGRVSWIKLARTKLKTSPHPHELT 324	Qy 264 FNKKR 	264 FNKRALOGPHR-PTGIASLAFSNOTTLAIASSYNTBHODT 304 281 OTKKITGRENDOVKIACHO-LICLAFSDT 315
à a	281 SLAFSNOGTLAIASSYNYBNODTEHPEDGIFTRQYTDAETKP 323 325 CCDW4SSGAFLYPALGYDMSRQHEDGWTQPGSKLYLHKCLEDMKPRP 370	RESULT 9 S71241 Probable RNA export	RSULT 9 871241 probable RWA export protein - Arabidopsis thallana
RESULT 8 839654 cell cycl NiAlterna C; Species C; Date:	RESULT 8 BASILT 19. 10. 19. 19. 19. 19. 19. 19. 19. 19. 19. 19	Species: Analogopais us Cipate: 28-0ct-196 Request Accession: 571241 Riccodman, H.M.; Gallant, Smartied to the EWBL Data A:Description: 47-5 Kb s A:Description: 47-5 Kb s A:Accession: 571240 A:Accession: 571240 A:Accession: 571240 A:Accession: 571241	Chaptass, Angelandona winather misses of the transport of the control of the cont
A;Title: A;Refere A;Access A;Molecu	Artitle: Saccharomyces cerevisiae genes required for cell cycle arrest in response to lo Affictence number: A39654; NUID:91330299; PMID:1651171 Affocession: B39654 Arresticus: 1-341, 4007	A;Cross-references: C;Generics: A;Introns: 19/3; 46 C;Superfamily: unaf F;68-101/Domain: WE	\(\)\(\)\(\)\(\)\(\)\(\)\(\)\(\)\(\)\(\
A,Cross- R,de Haa submitte A;Refere	Ciscoss references GBN644707, NID:9271136; PIDN:AAA34459.1; PID:9271137 Ride Haan, M.; Marrse, A.C.; Grivell, L.A. A:Reference number: Sector Date Library, May 1995	Query Match Best Local Simil: Matches 86; Cc	Query Match 19.9%; Score 352.5; DB 2; Length 251; DB 25 and 25 an
A, Access A; Molecu A, Residu A, Cross-	Ardension; 25-946-24 Ardicoule type: DM Ardicoule type: DM Ardicoule type: DM Ardicouse: Edecences: DMBLX887331; NID:g1041662; PIOM:CAA60742.1; PID:g829136	Qy 4 SNEF : :: Db 15 NKSYE	4 SNEPKINOPPEDGISSUKESPUTSOFILVASHOTSURLYDVPANSWRILKYQHTG 57 11 N.T. DI III 1 1 1 1 1 1 1 1
A; Experi R; de Haa submitte A; Refere	Apperimental Jource: strain 2888C A.C. Ride Haar, W.; GTVWEIL, L.A.; Makase, A.C. Almbitted for the Procein Sequence Database, July 1996 AlReference number: Sectin Sequence	Oy 58 AVLDO 1) Db · 74 PVLCS	Se Aviocaeve-Tahassalohqi.odib-Larogeii.verhbari.acverceevanviros 115
A, Access A, Molecu A, Residu A, Cross	Arkension; sessiva Arkantenia cypa; unwa Talicosa: roferances (BMsi. 174934; MID:g1420136; PIDN:CAA99216.1; PID:g1420137; GSPDB:GNOC Arkstowniamental sources: strain 2388C	Qy 116 WDQTV : : Db 134 WDKTV	116 #ROCTIVALDERFPOLACTESOPERVILYSSOPELIASSAPELIASSAPELIASSAPTOCREE 1'S 11414141 1151414 11414 11
C,Genetics A,Gene: SG A;Cross-re	Chempicse; A/Genes: SGD-BBB3, MIPS;YOROZéw A/Crose-references; SGD:SONOS552; MIPS:YOROZéw	0y 176 SSLKI Db 194 SPLKI	176 SELAYOTICCIARPHYGOYVISSIBERIAVBYIDESPEUGKKKYREKCHRIKEKANIEG 233
A, map post C; Function A, Descript: C; Superfam C; Keywords	deep boatstan 19x C;Function: eel cycle arrest C;Superfamily: eel cycle arrest protein BUB3 C;Superfamily: eel cycle control	Qy 234 IYPVN Db 225	234 IYPUNJISHHIHMTRATGGSDGFWINDPRNKKALOOF 272
Query Best L Matche Qy	Ouery Match Base Local Similarity 30.1%; Score 356; DB 1; Length 341; Base Local Similarity 50.1% Pred No. 79-6-23; Matches 103; Conservative 57; Mismatches 106; Indels 76; Gaps 15; 8 KLAQPPEDGISSVKRSEWTSOPLIVSSMINTSVRLYDVPANSMRLKYGHTGAVLD 61	RESULT 10 702818 polyA export protei CiSpecies: Leishmar CiDate: 24-Mar-1999	RESULT 10 polyA export protein PAXP [imported] - Leishmania major (strain Friedlin) polyA export protein and prote
8 & 8	s oriowernisorialieke-LLirakossirvikrebiokavoudosikkid	CJACCESSION: FS145) RIMYLET, P.J., Aud Proc. Natl. Acad. W Artile: Leishmani: A;Reference number A;Accession: F81458	Accession: Fainsy Tuests Tuests (C.) Address, C.; Magness,

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WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
Species: Notice sp. PCC 7120
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Species: Notice sp. PCC 7120
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C.Species: Nostoc sp. PCC 7120 PCC 7120
C.Dstreen Nostoc sp. PCC 7120 PCC 7120
C.Dstreen Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C.Dstreen 14-Dec-2001 #Sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C.Accession: A12155
                                     1010 LQGHTSCVRSVVFSPDGAMLASGGDDQIVRLMDISSGNCLYTLQGYTSWVRFLVFSPNGV 1129
                                                                                                                                                                                                                                                                         1130 TLANGSSDQIVRLWDISS-----KKCLYTLQGHTNWVNAVAFSPDGATLASGSGDQTVRL 1184
                                                                                                                                                                                                                                                                                                                                                                                                                         149 RLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRAFP-NKQGYVLSSIEGRVAVEY 207
                                                                                                                                                                                                                                                                                                                                                                    208 LDPSPEVOKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNTFATGGSDGFVNIWDPFNKK 267
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 -SMRLKYQHTGAVLDCAF-----YDPTHANSGGLDHQLKMHDLN-TDQENLVGTHDAPIR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           755 IATAGWDKTVKIWS-----IDGRLQKTLTGHTSGINSVTFSPDGKLIASASWDNTVKIW 808
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12.1%, Score 215, DB 2, Length 934;
Best Local Similarity 26.1%, Pred, No. 3.9e-10;
Matches 90, Conservative 55, Mismatches 122, Indels 78, Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1234 CLCTFQGHTSWWNSVVFNPDGSMLASGSS 1262
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A.Status; preliminary
A.A.Residuse; 1-339 «PR)
A.Gross-references: GB:ABC001274; NID:92264850; PIDN:AAC24641.1; PID:91407726; GSPDB:GN00
A.Gross-references: Strain MGOM/IL/81/Friedlin
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Kaneko, T.; Nakamura, Y., Molk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi
Makozaki, N.; Shimmo, S.; Sugimoto, M.; Takazasa, M.; Yameda, M.; Yasada, M.; Tabata,
DNA Res B. 276-212; 200-200.

DNA Res B. 276-212; 200-200.

A.Reference mumber: Alsibory, MUD:21595285, PMID:1175949
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C.Species; Noscoo sp. PCC 7120 is a gyronym of Landaean sp. strain PCC 7120
Cybete: Nostoo, sp. strain PCC 7120 is a gyronym of Landaean sp. strain PCC 7120
Cybete: il-Dec_200; Heaquence_tevision 14-Dec_2000 Heav. Change 0-Dec_2002
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12.99; Score 228; DB 2; Length 1526;
12.8milarity 25.88; Preced No. 5.7e-11;
85; Conservative 57; Mismatches 12.1; Indels 66; Gape 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50, Gaps 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                951 VRSVVFSPN-SLMLASGSSDQTVRLWDISSGECLYIFQGHTGWVYSVAFNLDGSMLATGS 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 FYDPTH------AWSGGLDHQLXMHDLNTDQENLVGTHDAPIRCVEY--CPE 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 INSOMLITGSWOGKLRWWDLROOSYVREENLGEPVFALDAOKTVPMMAAATGRLAHVYDV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 RNWGYVQQ-RRESSLKYQTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 QQMQKVNELKLPDVMKPNLRCITCAPQYDGVGVGSSEGRVSF1SMKDAPGC----TFKA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicharus proliminary
A.Wolconie Vype DAN
A.Rosdomes 1.158 GKURS
A.Cross-references: GS:RAN00019; PIDN:BAR75165.1, PID:GJ7132599, GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 -- PRIPCNAGIFSQPEK------SVSGD 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AWITTHDSPLLIMSFSADGRVFFGGCSKTAVMWDLNSNQKAVVASHDLPISCLDFLTLPQ 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 V -- NVMVTGSWDQTVKLWDPRIPCNAGIFSQPEKVYTLSVSGD-RLIVGTAGRRVLVWDL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 HRLKENNIEQIYPVNAISFHNIHNTFAIGGSDGFVNIWDPFNKKRL----CQ----FHRY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 HITTEKSHYILSQINPCVHHPILPLLLSGGGDGNLTVINRADRKVIKTLQCEQKVGTQAI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 LDHQLKMHDLNTDQ-BNLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWD----- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 EFKLNQPPEDGISSVKFSPNTSQFLL--VSSWDTSVRLYDVPANSMRLKYQHTGAVLDCA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 DHRLEATTSDCVSSVCFSPKECPMLMTGVASWDGSCSIWQVARNP-----AGAVISQP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 ISSVKFSPNTSQPLLVSSWDTSVRLXDVPANSMRLKYQ-HTGAVLDCAF-YDPTHAWSGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 PISAGDI--SADGSLVAYAHSYDWAMGKSG-----YRNQPTSVHIRPLS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 PTSIASLAFSNDGTTLAIASSYMYEMDDTBHPBDGIFIRQVTDAETKPKS 325
                                                                                                                                                                                                                                                                                                                              A.Gene: PAXP
A.HMP position: 1
7.Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 15.3%; Score 272; DB 2; Length 339 1 Similarity 25.7%; Pred. No. 1.39-15. Indels 90; Conservative 56; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 90; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: AC2239
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C.Species Ashidopsis thaliana (COSee are cress)
C.Species Ashidopsis thaliana (GOSee are cress)
C.Species (2-Webidopsis Mesquence_revision 02-Mar-2001 #text_change 02-Nov-2001
C.Accession: M86222 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
C.Accession: M86222 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
C.Accession: M86222 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
C.A. Francoin: A. D. Ever, J. P. Pale, Comway, A.B.; Comway, A.B.; Corway, A.R.; Crees; K.M.
Anthores Mander, J.L.; Chan, C. Comway, A.B.; Comway, A.B.; Comway, A.B.; Comway, A.B.; Marit. R.; Marzial M.A. Millor, J. M.; C. M.; L.; Schwartz, J. B.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
A.Authores Salaberg 5. L.; Schwartz, J. B.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon
A.Titles Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A.Accession: M86222
                      .067 TDPQGMIMSVAFSLDGTLLASASEDQTVKLWNLKTGECVHTLKGHE-KQVY---SVAFSP 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1123 NGQIAASGSEDTTVKLWDISTGSCVDTLKHGHTAAİRSVAFSPDGRLLASGSEDEKIQLW 1182
                                                                                                                             131 AGTFSQPEKVYTLSVSGDRLIV--GTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRAF 188
                                                                                                                                                                                                                                                                     189 PNKQGYVLS---SIEGR-VAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISFHN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 AVLOCAFYDP-THAMSGGLDHQLKMHD-LNTDQENLVGTHDAPIRCVEYCPEVNVMVTGS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SNEFKLNOPPEDGISSVKFSPNTSOFLLVSSWDTSVRLYDVP-----ANSMRLKYQHTG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005172; NID:98927663; PIDN:AAF82154.1; GSPD8:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                         245 IHNTFATGGSDGFVNIWDPFNKKRLCQF-HRYPTSIASLAFSNDGTTLA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 140;
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                                                                                                                                                                                OKLKGHSHWWTVAFSPDGRILASGSADSEIKIWDVAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1183 DMQNCSRLKTLKSPRLYENMDITD-----ITGITDAE 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----IASSYMYE-MDDTEHPEDGIFIRQVTDAE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 198.5; DB 2
Pred. No. 7.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch
1 Similarity 35.7%; Pred. No. 7.9e-
45; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: November 12, 2003, 20:10:46
Job time : 21 secs
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-140 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293
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WD-40 repeat procein (imported) - Nostco sp. (strain PCC 7120)

A.McDer Mostco sp. strain PCC 7120

A.McDer Mostco sp. strain PCC 7120

A.McDer Mostco sp. strain PCC 7120

G.Accession: Angle dequence_revision 14-Dec-2001 #text_change 09-Dec-2002

G.Accession: Angle Mostco sp. strain PCC 7120

G.Accession: Angle Mostco sp. sugimence, M.; Takazawa, M.; Yamada, 
Kanneko, T., Nakemura, Y.; Wolk, C.P.; Kurita, T.; Sesamoto, S.; Watanabe, A.; Iriguchi
Nakazaaki, V.; Shimpo, S.; Sugimoto, N.; Tahazaaw, M.; Yamada, M.; Tabata, S.
A;Ttle: Complete Genome, Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Accession, AIZ155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11,
                                                                                                                                                                                                                  A.Status; preliminary
A.Holeaule type. 1.128 «KUR»
A.Residues: 1.128 «KUR»
A.Foresimentel Serrores: GERADONO19; PIDN:BAB74499.1; PID:g17131893; GSPDB:GN00179
A.Forestimentel source: greatin POC 7120
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947 DRQILASGSNDKTVKLMPWQTGKYISSLEGHTDFIYGIAFSPDSQTLASASTDSSVRLWN 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .007 ISTGOCROLLEHIDMVY---AVVFHPQGKIIATGSADCTVKLMNISTGQCLKTLSEHSD 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 GGLDHQLKWHDLNTDQ--ENLVGTHDAPIRCVEYCPEVNVMYTGSWDQTVKLWDPRTP-C 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 NAGTESQPEKVYTLSVS--GDRLIVGTAGRRVLVMDLRN----------MGYVQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 887 IKTLHGHTNEVCSVAFSPDGQTLACVSLDQSVRLWNCRTGQCLKAWYGNTDWALPVAFSP 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 ----KCHRLKENNIEQIYPVNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPT 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVLDCAFY-DPTHAWSGGL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGISSVKFSPNTSQFLLVSSWDTSVRLYDV-PANSMRLKYQHTGAVLDCAF-YDPTHAMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 ORRESSLKYQTRCIRAFPNKQGYVLSSIEGRVAVEY-LDPSPEVQKKKYAF-----
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1 Similarity 24.8%; Pred: No. 31.26-09;
1 Similarity 24.8%; Pred: No. 31.26-09;
24.8%; Conservative 61; Mismacches 13.1 Indela 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 209; DB 2; Length 1258;
llarity 24.5%; Pred. No. 1.9e-09;
Conservative 60; Mismatches 139; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1064 KILGMAWSPDGQLLASASA 1082
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ses 78; Conserv
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Best Local Similarity
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A,Gene: alr2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Si
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1. (2010) Godden_4 (genesed_7 emb) (AA1980_DRT**

2. (2010) Godden_4 (genesed_7 emb) (AA1980_DRT**

2. (2010) Godden_4 (genesed_7 emb) (AA1981_DRT**

3. (2010) Godden_4 (genesed_7 emb) (AA1981_DRT***


4. (2010) Godden_4 (genesed_7 emb) (AA1981_DRT***


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4. (2010) Godden_4 (genesed_7 emb) (AA1
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                Polynucleotides encoding a cancer associated human protein kinase BUB3 (huBUB3) protein, useful for the prevention, diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNA1
                                                                                                                                                                                                                                                                                                         The invention relates to cancer associated human protein kinase BUB3
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neoplastic tissue; neoplasia; kinase; cytostatic; kinase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1772; DB 23; Length 328; 100.0%; Pred, No. 1.1e-177;
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                                                                                                                                                                                                                                                        Claim 1; Column 49-52; 47pp; English.
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                                         This sequence represent human Bins, a procein that conclusors with prints sequence represent human Bins, a procein that conclusors with procein conclusions and substant bloom of these kinases. The BUBB procein comprol, BUBB, is a substrate lay a pivosal role in microic checkforin comprises 5 MP-40 monit respeats. It Cocalises to the Kintochoneva during microsis. BUBB rolls (see a MASSBOY) was isolated from a human EST database, with additional sequences obtained by STARCE. BUB genes (see AMASSBOY-XI) and their exquences obtained by STARCE. BUB genes (see AMASSBOY-XI) and their valuable their expension to targets for the design of antiporification observed in the unwant cells, whicholdes and objanual colleging based on any are also useful in screening for therapeutics, disponsis and
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Claim 32; Page 94~95; 99pp; English.
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                                                                                                                                                                                                                                                                                                                                                                          This invention relates to an isolated and purified husDB3 protein which is involved in cell Cycle control and appropries. The invention also comprises a method for diagnosing a neoplosis. The invention and a method for a diagnosing a neoplosis or progress of neoplasis in a human, and a method for a diagnosing or progress of neoplasis in a human. Also disclosed are methods for identifying compounds which human. Also disclosed are methods for identifying compounds which protein of the invention may have cyclosisatic activity and the DBA protein of the Almeriton may have cyclosisatic activity and the DBA sequence enoding it may be used in matteened entrapy as a kinsee inhibitor. The methods and compositions are useful more than adjustic and accorded of discretely such activity betain of discretels with methods of the human bush protein used in the methods of the invention of the invention are second.
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                                                                                                                                                                                                                                                                                     New isolated and purified huguss protein, useful for the diagnosis and
treament of disorders with mutation of the huguss protein, such as
cancer of the lung, breast, colorectal, bladder, prostate, liver or
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                                                                                                                                   97US-068102P.
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                                                                                              27-FEB-2002; 2002US-0084700.
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Best Local Similarity 100.0
Matches 328; Conservative
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                                               US2002160403-A1.
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No. 1.28-177. Metches 338; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer associated protein sequence SEQ ID NO:1301.
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AAB43856 standard; Protein; 332 AA.
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61 DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
                                                                                                                                                                                                                                               61 DCAFYDPIHAMSGGLDHQLRWHDLNTDQENLVGTHDAPIRCVEYCFEVNVMVTGSWDQTV 120
                                                                                                                                                                                                                                                                                                                                    121 XLWDPRTPCNAGTFSQPEKYYTLSVSGDRLIVGTAGRRVLVWDLRNWGYVQQRRESSLKY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SPHNIHNTFATGGSDGFVNIMDPFNKKRLCGFHRYPTSIASLAFSNDGTTLAIASSYWYE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic and detection reagent capable of detection to an isolated nucleic and of detection in the invention is useful in developmental biology and in elucidating cell islandling and cell-cell interactions in higher elektroies for the development of inserticides, therapeutics and pharmicounical drugs. The invention discloses genome: DN asserticides, therapeutics and pharmicounical drugs. The invention sequences (ABLOS) and the encoded processed DNA sequences (ABLOS) and the encoded processed DNA
                                                                                                                                                                                                                                                                                                           KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY 180
                                                                                                                                                                                                                                                                                                                                                                                                             QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ÖTRCIRAFPNKÖGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQITPVNAI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SFHNIHNTFATGGSDGFVNIWDPFNKKRLCOFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
                                                                                                     1 MTGSNEFKLNOPPEDGISSVKFSPNTSOFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from brosophila and for elucidating cell signalling and cell-cell
                                                                                                                                     1 MTGSNEFKLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSWRLKYQHTGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila, developmental biology, cell signalling, insecticide;
Query March 99.5%; Score 1763; DB 20; Length 328; Best Local Similarity 99.7%; Pred. No. 10-176; Metches 321; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, SEQ ID NO 4341; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 4341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 MDDIEHPEDGIFIRQVTDAEIKPKSPCT 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABBS9183 standard; Protein; 326 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             245 SFHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTAIASSYMYE 304
                                                                                                         61 DCAFYDPTHAWSGGLDHQLXMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
                                                                                                                                                     65 DCAFYDPTHAWSGGLDHQLKWHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 124
                                                                                                                                                                                                                                                                                                                                                                                                             241 SFHNIHNTFATGGSDGFVNIMDPFNKKRLCOFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
                                5 MTGSNEFKLNOPPEDGISSVKFSPNTSQFLLVSSMDTSVRLYDVPANSMRLKYQHTGAVL 64
        1 MTGSNEFKLNOPPEDGISSVKFSPNTSOFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the mains oxid sequence of himan hinging procein. A new hinging horelar oxid sequence of himan hinging procein. A new hinging and the hinging sequence oxid the hinging hinging the research oxid the hinging the fall mass activity. The hinging gene (see ANYA172) is muched in cancer cells. Agents that finerfere with hubidi-hubidis interaction, or which reduce hinging that finerfere with hubidi-hubidis interaction, or which reduce hinging oxid ficting and to interact the research or which reduce hinging that cancer agents, but the timours to attach cancer agents, or to treat other hyperproliferative diseases
                                                                                                                                                                                                                                                                                                               OTRCIRAFPNKOGYVLSSIEGRVAVBYLDPSPEVOKKKYAFKCHRLKENNIEOIYPVNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wew human BUB1 protein - useful for diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BUB1, huBUB3; human, huBUB1; cell cycle; apoptosis; tumour; cancer; neoplasia; psoriasis; diagnosis; therapy.
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97US-0049068.
97US-0068102.
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328 AA;

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99US-0137528.
99US-0137502.
99US-0137724.
99US-0138094.
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99US-0139454.
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99US-0134219.
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99US-0144814
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     66 DPTHAMSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLMDP 125
                                                                                                                                                                                                                                                                         65 DIVHVVSGSLDNQLRLFDVNTQAESIIGAHEFPIRCVEHAEYVNGILTGSMDNTVKLWDM 124
                                                                                                                                                                                                                                                                                                                      126 RTPCNAGTFSQPE-KVYTLSVSGDRLIVGTAGRRVLVWDLRNWGYVQQRRESSLKYQTRC 184
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                                                                                                                                                                                                                                                                                                                                                                                                         6 EFKLINGPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVLDCAFY 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     procein identification, signal transduction pathway, metabolic pathway, 
pryvidiserion assay, genetic mapping, gene expression control, promoter; 
termination sequence.
     (Albabaya)-Abayav202).
The sequence data for this patent did not form part of the printed appetification, but was obtained in electronic format directly from WIPO at the Alpoint publybublished pot_sequences.
                                                                                                                  Owery Match 59.3%; Score 1050.5; DB 22; Length 326; Best Local Similarity 60:48; Pred. No. 1.18-101.] Indels 3; Gaps Matches 195; Conservative 49; Mismatches 75; Indels 3; Gaps
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                                                                                       Seguence 326 AA;
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09-MAR-1999;
23-MAR-1999;
25-WAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
119-APR-1999;
21-APR-1999;
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28-APR-1999;
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AAG33215;
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                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                   07-JUN-2001; 2001WO-US18569.
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Protein identification; signal transduction pathway, metabolic pathway, 
prychidsation asawy; genefic mapping; gene expression control; promoter; 
termination sequence; corn.
                            Zea mays protein fragment SEQ ID NO: 40212.
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                                                                 Zea mays subsp. mays.
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
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AAG33215 standard; Protein; 343 AA.

RESULT 9 AAG3321S ID AAG

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203 VAVEYLDPSPEVQKKKYAPKCHRLKENNIEQIYPVNAISFHNIHNTFATGGSDGFVNIMD 262
                                                           61 VAMEFFDLSEAAQAKKYAFKCHRKSEAGRDIVYPVNSIAFHPIYGTFATGGCDGFVNIWD 120
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pyvytidsation, assay; genetic mapping; gene expression control; promoter;
termination sequence.
1 MSLVGHRLVVATAGRHVNIYDLRNMSQPEQRRBSSLKYQTRCVRCYPNGTGYALSSVEGR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 3475.
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| 337528.<br>337754.<br>33874.<br>338874.<br>338874.<br>338875.<br>33952.<br>33952.<br>33955.                                                                                                  | 139467.<br>139468.<br>139468.<br>139468.<br>139468.<br>139468.<br>139968.<br>139968.<br>13968933.<br>1406356.                                                                                                         | 9905.0141287<br>9905.0141287<br>9905.0141842<br>9905.0141842<br>9905.0141842<br>9905.0141055<br>9905.014105<br>9905.0141803<br>9905.0141803<br>9905.0141803<br>9905.014183<br>9905.0141313<br>9905.0141313                                                                                                                                                                                                                                                                                                                                                                                                      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Score 578.5; DB 21; Length 349;

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 S8 AVLDCAFYDP-THAMSGGLDHQLKMHD-LNTDQENLVGTHDAPIRCVEYCPEVNVMVTGS 115
 116 WDQTVKLWDPRIPCNAGIFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRE 175
 SSLKYQTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIY 235
 236 PUNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIAS 295
 248 SVNSLNFHPVHGTFATAGSDGAFNFWDKDSKQRLKAMSRCNQPIPCSSFNHDGSIYAYAA 307
 4 SNEFKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVP-----ANSMRLKYQHTG 57
 Protein identification; signal transduction pathway; metabolic pathway; whyridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
 19; Gaps
Best Local Similarity 38.7%; Pred. No. 5.8e-52;
Matches 129; Conservative 60; Mismatches 125; Indels
 Arabidopsis thaliana protein fragment SEQ ID NO: 56906.
 296 SYMYEMDDTEH----PEDGIFIRQVTDAETKPK 324
 308 CYDWSKGAENHNPATAKSSIFLHLPQESEVKAK 340
 AAG45336 standard; Protein; 349 AA.
 990S-012834
990S-012834
990S-012874
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990S-0130891
990S-013089
990S-0132048
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 99US-0132484.
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99US-0132486.
 25-FEB-2000; 2000EP-0301439
 99US-0123548
99US-0125788
 99US-0132487.
 90S-0134256
 18-OCT-2000 (first entry)
 Arabidopsis thaliana
 22 - FEB 1999

05 - WR 1999

10 - WR 1999

23 - WR 1999

23 - WR 1999

10 - WR 1999

10 - WR 1999

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 BP1033405-A2
 36-SEP-2000
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990S-0145276.
990S-0145913.
990S-0145918.
990S-0145919.
990S-0145951.
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 12-AUG-1
 20-AUG-
 17-AUG-
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176 SSLKYQTRÇIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIY 235
 194 SPLKYQTRCVTAFPDQQGFLVGSIEGRVGVHHLDDSQ--QSKNFTFKCHR--DGN--DIY 247
 236 PVNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIAS 295
 248 SVNSLNFHPVHGTFATAGSDGAFNFMDKDSKQRLKAMSRCNQPIPCSSFNHDGSIYAYAA 307
 116 WDQTVKLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRE 175
 4 SNEFKLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVP----ANSMRLKYQHTG 57
 15 NKSYBVTPSPADSISSLSFSPR-ADILVATSWDNQVRCWBISRSGASLASAPKASISHDQ 73
 Human, secreted protein; EST, expressed sequence tag, diagnosis; foremais, gene therapy, chromosome mapping; signal peptide; upperceam regalactory sequence; oycohia activity, cell proficeration; differentiation, hematopoiseis regulation; tisaue growth regulation; expenductive hormor regulation; of memoractic, themakinetic; haemostatic; thrombolytic; anti-tiffammatory; tumour inhibition.
 58 AVLDCAPYDP-THAWSGGLDHQLXOMD-LNTDQENLVGTHDAPIRCVEYCPEVNVWVTGS
 32.6%; Score 578.5; DB 21; Length 349;
38.7%; Pred. No. 5.8e-52;
ive 60; Mismatches 125; Indels 19; Gaps
 296 SYMYEMDDTEH ----PEDGIFIRQVTDAETXPK 324
 308 CYDWSKGAENHNPATAKSSIFLHLPQESEVKAK 340
 Duclert A, Dumas Milne Edwards J, Lacroix B;
 Human 5' EST secreted protein SEQ 1D NO:364.
 AAY12333 standard; Protein; 107 AA
 9905-0161404
9905-0161405
9905-0161359,
9905-0161350,
9905-0161361
9905-0161361
9905-0161950
9905-0161992
9905-0161933
 99US-0160989
 98WO-IB01222
 97US-0905135
 17-JUN-1999 (first entry)
 Best Local Similarity 38.79
Matches 129; Conservative
 (GEST) GENSET
 01-AUG-1997;
22-0CT-1999;
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28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
 Homo sapiens.
 31-JUL-1998;
 WO9906548-A2
 11-FEB-1999.
 AAY12333;
 Query Match
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 AAY1233.
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WPI; 1999-153778/13

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invention is
 60 LD-CAPYDPTHAWSGGLDHQLKWHDLNTDQENLVGTHDAPIRCVEYC--PEVNVMVTGSW 116
 72 LDVCWSDDGSKVFVASCDKQVKLWDLASDQVMQVAAHDGPVKTCHMVKGPTYTCLMTGSW 131
 117 DQTVKLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRES 176
 132 DKILKFWDTRSPNPMYTINLPERCYCADVEYPMAVVGTANRGLIIYSLQNSPTEYKRQES 191
 192 PLKYOHRAISIFRDXKKEPTGCALGSIEGRVAIQYVNPGN--PKDNFTFKCHRTTGTSGY 249
 177 SLKYQTRCIRAFPNKQ----GYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLK-ENNI 231
 232 BQIYPVNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTL 291
 5 NEPKINOPPEDGISSVKFSPNTSQ--FLLVSSWDTSVRLYDVPANSMRL-KYQHT--GAV 59
 12 NDFEVASPPDDSVSALEFSPSTVQKNFLVAGSWDSTVRCWEVEQNGATVPKSMKTMGGPV 71
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at trp, wipo, into publybublished pot_sequences.
genes from Drosophila and for elucidating cell signalling and cell-cell
 The invention relates on a isolated nucleic caid detection resident
to the detecting 1000 or more gene from possobhila. The invention
useful in developmental biology and in situadiating end is signalling and
insecticide, therepactions in higher enkaryotes for the development of
insecticides, therepactice and paremaceutical drugs. The invention
discusse genomic DNA sequence (ABLIATE) and the encoded protein expressed DNA
engaryors. ARBIOISHOUSE.
 Transport-associated protein, TRAMP, nuclear pore, nuclear transport, wastel trafficking fanner, cystic fibrosis, multidrug resistance; hypercholesterolaenia; diagnosis, treatment
 Gaps
 23;
 Query Match

29.4%, Score 521.5; DB 22; Length 346;
Best Local Smilarity 36.4%, Pred. No. 58e.46,
Matches 123; Conservative 59, Mismatches 133; Indels 23;
Matches 123; Conservative 59
 /note= "Beta transducin family Trp-Asp repeat"
144.158
/note= "Beta transducin family Trp-Asp repeat"
 Disclosure, SEQ ID NO 20931; 21pp + Sequence Listing; English
 310 AYAVGYDWSKGHEYFNPAKKPO--IFLRSCYD-ELKPR 344
 292 AIASSYMYE-----MDDTEHPEDGIFIRQVTDAETKPK 324
 Human transport-associated protein-9 (TRANP-9).
 Location/Qualifiers
 AAY31647 standard; Protein; 368 AA
 02-NOV-1999 (first entry)
 346 AA;
 WO9941373-A2.
 Homo sapiens
 interactions
 19-AUG-1999
 Sequence
 AAY31647;
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 1 MTGSNEFKINQPPEDGISSVKFSFNTSQFLIVSSWDTSVRLYDVPANSMRLKYQHTGAVL 60
 1 MTGSNEFKLNQPPEDGISSVKFSPNTSQFLLVSSMDTSVRLYDVPANSMRLKYQHTGAVL 60
 New isolated nucleic acid detection reagent for detecting 1000 or more
 0; Gaps
 AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
 New nucleic acids encoding human secreted proteins - obtained from Thomas prepared from e.g. liver, overy, brain, prostate, kidney, ling, umblical cord, placenta and colon tissue
 Drosophila, developmental biology, cell signalling, insecticide,
 Score 571; DB 20; Length 107;
Pred. No. 6e-52;
0; Mismatches 2; Indels (
 61 DCAFYDPTHAWSGGLDHXXXMHDLNTDQENLVGTHDAPIRCVEYCP 106
 61 DCAFYDPTHAWSGGLDHQLKWHDLNTDQENLVGTHDAPIRCVEYCP 106
 Drosophila melanogaster polypeptide SEQ ID NO 20931.
 Myers EW;
 ABB64713 standard; Protein; 346 AA.
 Claim 27, Page 697; 824pp; English.
 Li PWD,
 Query Match
Best Local Similarity 98.1%;
Matches 104; Conservative (
 23-MAR-2001; 2001WO-US09231.
 23-MAR-2000, 2000US-191637P.
 26-MAR-2002 (first entry)
 Drosophila melanogaster.
 Venter JC, Adams M,
 WPI; 2001-656860/75.
 (PEKE) PE CORP NY
 107 AA;
 N-PSDB; ABL08816.
 N-PSDB; AAX41166.
 WO200171042-A2.
 pharmaceutical
 27-SEP-2001
 Sequence
 ABB64713;
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the DRN Sequence reposetts name ritingport associated processory (IRANE'S).

THE DRN Sequence was 1.1 and (LEADNA 1.4 as to a total food settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of settson of control of control of settson of control of contro
 nice descent mountaining to hyporenesion TRANPy as expressed in cancer colls and transport disorders result from either excessive or cincils insufficient molecular transport. Anii TRANP multibodies and multide acids encodaing TRANP can be used to treat or prevent a center sesciotated with increased TRANP expression. Anti-TRANP antibodies can be used discertified as an antagonist or as a targetting mechanism for drugs. Alternatively, as TRANP mitisense mucleotide can be used to treat conneces. A TRANP adopted transport of Pladogically acids weed to treat cancers.
 This sequence represents human transport-associated protein-9 (TRANP-9).
 Human TRANP coding sequences, used to treat transport disorders and
 Bandman O, Baughn MR, Corley NC, Guegler KJ;
Lal P, Yue H;
 Claim 1; Page 77-78; 87pp; English.
99WO-US02527.
 98US-0021764.
 (INCY-) INCYTE PHARM INC.
 WPI; 1999-508646/42.
 N-PSDB; AAZ11739.
05-FEB-1999;
 11-FEB-1998;
 Au-Young J,
Hillman JL,
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91 DVCMSDDGSKVFTASCDKTAKMMDLSSNQAIQIAQHDAPVKTIHWIKAPNYSCVMTGSWD 150 61 D-CAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEY -- CPEVNVMVTGSWD 117 118 QTVKLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESS 177 178 LKYQTRCIRAFPNKQ----GYVLSSIEGRVAVEYLDPSPEVQKKKXAFKCHRLKENNI-- 231 232 -EQIYPVNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTT 290 270 PQDIYAVNGIAFHPVHGTLATVGSDGRFSFWDKDARTKLKTSEQLDQPISACCFNHNGNI 329 31 DIEVTSSPODSIGCLSFSPPTLPGNPLIAGSWANDVRCWEVQDSGQTIPKAQQMHTGPVL 90 6 EFKLNOPPEDGISSVKFSPNT--SQFLLVSSWDTSVRLYDVPANSM---RLKYQHTGAVL 60 61; Mismatches 141; Indels 20; Gaps 28.7%; Score 509; DB 20; Length 368; 34.3%; Pred. No. 1.3e-44; 291 LAIASSYMYEMDD---TEHPEDGIFIRQVTDAETKPKS 325 Query Match
Best Local Similarity 34.3
Matches 116; Conservative 368 AA; Sequence 셤 g ò à 윱 ò 윱 ò ŝ 윱

330 FAYASSYDWSKGHEFYNPQKKNYIFLRNAAE-ELKPRN 366

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Search completed: November 12, 2003, 20:08:49 Job time : 44 secs

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November 12, 2003, 20:07:58; Search time 21 Seconds (whthout alignments) 660.855 Million cell updates/sec
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and is derived by analysis of the cotal score distribution.
 1 MIGSNEFKLNQPPEDGISSV......DGIFIRQVIDAETKPKSPCT 328
 328717
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 328717 segs, 42310858 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1772
 BLOSUM62
 Title:
Perfect score:
 Scoring table:
 Database :
 Seguence:
 Searched:
 Run on:
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|            | tion         | 4               | 157               | _                 | 13,              | 'n              | ice 1, Appli    | 12,               | 12,              | 38,               | 38,              | 38,              | ice 38, Appl      | .,              | ice 18, Appl     | 18,              | 33,               | 33,              | 33,              | 33,               | 63,               | 63,              | 63,              | 63,               | ice 3, Appli    | 42,               | 42,              | 42,              |
|------------|--------------|-----------------|-------------------|-------------------|------------------|-----------------|-----------------|-------------------|------------------|-------------------|------------------|------------------|-------------------|-----------------|------------------|------------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-------------------|-----------------|-------------------|------------------|------------------|
|            | Description  | Seguence        | Sequence          | Sequence          | Sequence         | Sequence        | Sequence        | Sequence          | Sequence         | Sequence          | Sequence         | Sequence         | Seguence          | Sequence        | Sequence         | Sequence         | Sequence          | Seguence         | Seguence         | Seguence          | Seguence          | Seguence         | Seguence         | Seguence          | Sequence        | Sequence          | Sequence         | · Sequence       |
| SUMMARIES  | QI.          | US-09-095-881-4 | US-09-247-155-157 | US-09-291-170A-13 | US-09-724-884-13 | US-09-063-743-1 | US-09-590-540-1 | US-09-291-170A-12 | US-09-724-884-12 | US-08-190-802A-38 | US-08-477-346-38 | US-08-473-089-38 | US-08-487-072A-38 | US-09-245-039-1 | US-08-188-582-18 | US-08-646-715-18 | US-08-190-802A-33 | US-08-477-346-33 | US-08-473-089-33 | US-08-487-072A-33 | US-08-190-802A-63 | US-08-477-346-63 | US-08-473-089-63 | US-08-487-072A-63 | US-09-108-857-3 | US-08-190-802A-42 | US-08-477-346-42 | US-08-473-089-42 |
|            | 80           | 4               | 4                 | •                 | 4,               | м               | 4               | 4                 | 4                | -                 | m                | 4                | 4                 | 4               | -                | -                | -                 | e                | 4                | 4                 | н                 | 6                | 4                | 4                 | 4               | -                 | ٣                | 4                |
|            | Match Length | 328             | 29                | 251               | 251              | 375             | 375             | 250               | 250              | 340               | 340              | 340              | 340               | 340             | 704              | 704              | 318               | 318              | 318              | 318               | 713               | 713              | 713              | 713               | 713             | 340               | 340              | 340              |
| *<br>Ouerv | Match        | 100.0           | 14.6              | 11.1              | 11.1             | 10.0            | 10.0            | 9.6               | 9.6              | 9.6               | 9.6              | 9.6              | 9.6               | 9.6             | 9.6              | 9.6              | 9.4               | 4.6              | 9.4              | 9.4               | 9.5               | 9.5              | 9.2              | 9.2               | 9.2             | 1.6               | 9.1              | 9.1              |
|            | Score        | 1772            | 258               | 197.5             | 197.5            | 176.5           | 176.5           | 169.5             | 169.5            | 169.5             | 169.5            | 169.5            | 169.5             | 169.5           | 169.5            | 169.5            | 166               | 166              | 166              | 166               | 163               | 163              | 163              | 163               | 163             | 160.5             | 160.5            | 160.5            |
| Result     | NO.          | -               | 7                 | ٣                 | 4                | 'n              | 9               | 7                 | 80               | 6                 | 10               | 11               | 12                | 13              | 14               | 15               | 16                | 7.7              | 18               | 19                | 50.               | 21               | 22               | 23                | 24              | 25                | 26               | 27               |

RESULT 2 US-09-247-155-157

| Appl              | Appli           | Appli           | Appli           | Appli           | Appl              | Appl             | Appl             | Appl              | Appl              | Appl              | Appli           | Appl             | Appl             | Appl             | Appl             | Appl              | Appl              |  |
|-------------------|-----------------|-----------------|-----------------|-----------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|-----------------|------------------|------------------|------------------|------------------|-------------------|-------------------|--|
| 42,               | œ               | 4               | 4,              | 4,              | 39,               | 39,              | 39               | 39,               | 64,               | 68,               | ~               | 64,              | 68,              | 64,              | 68,              | 64,               | 68,               |  |
| Sequence          | Seguence        | Sequence        | Sequence        | Sequence        | Seguence          | Seguence         | Sequence         | Sequence          | Sequence          | Seguence          | Seguence        | Seguence         | Seguence         | Seguence         | Seguence         | Sequence          | Seguence          |  |
| US-08-487-072A-42 | US-08-914-999-8 | US-08-751-189-4 | US-09-060-836-4 | US-09-184-445-4 | US-08-190-802A-39 | US-08-477-346-39 | US-08-473-089-39 | US-08-487-072A-39 | US-08-190-802A-64 | US-08-190-802A-68 | US-08-308-818-2 | US-08-477-346-64 | US-08-477-346-68 | US-08-473-089-64 | US-08-473-089-68 | US-08-487-072A-64 | US-08-487-072A-68 |  |
| 4                 | 4               | ~               | ~               | m               | -                 | m                | 4                | 4                 | -                 | н                 | Ν               | e                | m                | 4                | 4                | 4                 | 4                 |  |
| 340               | 732             | 2629            | 2629            | 2629            | 326               | 326              | 326              | 326               | 198               | 798               | 798             | 798              | 798              | 198              | 798              | 798               | 798               |  |
| 9.1               | 9.1             | 6.9             | 8.9             | 8.9             | 8.8               | 8.8              | 8.8              | 8.8               | 8.7               | 8.7               | 8.7             | 8.7              | 8.7              | 8.7              | 8.3              | 8.7               | 8.7               |  |
| 160.5             | 160.5           | 158             | 158             | 158             | 156.5             | 156.5            | 156.5            | 156.5             | 155               | 155               | 155             | 155              | 155              | 155              | 155              | 155               | 155               |  |
| 58                | 53              | 30              | 33              | 35              | 33                | 34               | 35               | 36                | 37                | 38                | 39              | 40               | 41               | 42               | 43               | 44                | 45                |  |

## ALIGNMENTS

RESULT 1 US-09-095-881-4

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73 GSRDGTARLMNVAIGTEHAVLKGHTDYVYAVAFSPDGSMVASGSRDGTIRLMDVATGKER 132
 132 GTFSQP-EKVYTLSVSGD-RLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRAFP 189
 133 DVLQAPAENVVSLAFSPDGSMLVHGSDSTVHLWDVASGEALH-----TPEGHTDWVRAVA 187
 188 FSPDGALLASGSDDRTIRLWDVAAQEE------HTTLEGHTE---PVHSVAFHPEGTT 236
 190 -NKÇĞYVLSSIBGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNT 248
 131
 73 GSRDGTARLWNVATGTEHAVLKGHTDYVYAVAFSPDGSWVASGSRDGTIRLWDVATGKER 132
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 190 -NKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNT 248
 188 FSPDGALLASGSDDRTIRLWDVAAQEE------HTTLEGHTE---PVHSVAFHPEGTT 236
 15 DGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDCAFY-DPTHAWS 72
 73 GGLDHQLKMHDLNTDQENLV-GTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRTPCNA
 132 GTFSQP-BKVYTLSVSGD-RLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRAFP
 Ouery Match 11.1%; Score 197.5; DB 4; Length 251; Dest Local Similarity 27.1%; Pred. No. 2.1e.13; Matches 79; Conservative 48; Mismatches 112; Indels 23; Gaps
 OTHER INFORMATION: putative serine/threonine kinase PkwA WD40 repeat OTHER INFORMATION: region
 Sequence 13. Application US/09724684
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Waterman, James A
FULLOANT: HERMAN, James Car the University of California
APPLICANT: HERMAN, Sands for the Detection of Microtubule
TITLE OF INVENTION: Assays for the Detection of Microtubule
TITLE OF INVENTION: Assays for the Detection of Microtubule
TITLE OF INVENTION: BSST9-00051,035
GURRENT APPLICATION WHORE: US/09/124,884
GURRENT APPLICATION WHORE: US/09/124,884
FRIOR APPLICATION WHORE: 09/391,170
WHOMES OF SEGO ID NOS: 160-11.28
 TYPE: PRT
ORGANISM: Thermomonospora curvata
 Sequence 1, Application US/09063743
Patent No. 6242214
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 249 FATGGSDGFVNIW 261
 237 LASASEDGTIRIW 249
 249 FATGGSDGFVNIW 261
 237 LASASEDGTIRIW 249
 SOFTWARE: Patentin Ver. 2.0
 APPLICANT: Bandman, Olga
 US-09-724-884-13
 ; OTHER INFORM
US-09-724-884-13
 LENGTH: 251
 US-09-063-743-1
 SEQ ID NO 13
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 73 GGLDHQLKMHDLNTDQENLV-GTHDAPIRCVEYCPEVNVMVTGS#DQTVKLWDPRTPCNA 131
 15 DGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDCAFY-DPTHAMS 72
 Quety Watch 11.1%; Score 197.5, DB 4, Length 251, Best Local Stalatity 2.7% pred, No. 2.16-12, Indels 23, Gaps Matches 12, Indels 23, Gaps
 Gaps
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 Length 59;
 49 MRLKYQHTGAVLDCAFYDPTHAWSGGLDHQLXXHDLNTDQENLVGT 94
 Score 258; DB 4; L
Pred. No. 4.6e-21;
 ABRICANT INCRAFALING Edwards, Jean-Baptiste ABRICANT Dumes Milne Edwards, Jean-Baptiste ABRICANT Dumes Milne Edwards, Jean-Baptiste ABRICANT DUMESTON OF THE RESERVENCE OBSIGN CONSERVEY DUMS CHEEKER FILES RETURNERS, US/90/247,155A CHEEKER FILES OPETION DATE: 399-00-109
EARLIER FILES OPETION DATE: 399-00-10
EARLIER FILES FILES FILES FILES FILES FILES FILES FILES FILES BALLES FILES FI
 14.6%; Scor.
100.0%; Pred. No. 3...
Sequence 157, Application US/09247155A Patent No. 6312922 GENERAL INFORMATION:
 46; Conservative
 ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 46; Conservi
 , LOCATION: -22..-1
US-09-247-155-157
 NAME/KEY: SIGNAL
 FEATURE:
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66 EGEVYCCKFHPNGST-LASAGFDRLILLMNVYGDCDNYATLK-GHSGAVMELHYNTDGSM 123
 70 AWSGGLDHQLKOHDLNTDQ--ENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRT 127
 124 LFSASTDKTVAVMDSETGERVKELKGHTSFVNSCYPARRGPQLVCTGSDDGTGKLMDIRK 183
 128 PCNAGTFSQPEKV--YTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTR-- 183
 184 KAAIQTPQNIYQVLAVTFNDISBQIISGGIDNDIKVWDL,-----RQNKLIYTMRGH 234
 240 I--SFHNIHNTFATGGSDGPVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASS-296
 184 ----CIRAFPNKOGYULSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNA 239
 235 ADSVTGLSLSSEGSYLLSNAMON-TVRVWDVRPPAPKE----RCVKIFQGNVHN-FEKNL 288
 14 EDGISSVKFSPNTSQFLLVSSNDTSVRLYDVPA---NSMRLKYQHTGAVLDCAF-YDPTH 69
 37;
 Length 375;
 Patterson, Chandra
TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
 COMPUTER: IMP Compatible
OPERATING SYSTEM: DOS Windows Version 3.0
CURRENT PARE FastENCY for Windows Version 3.0
CURRENT PARE 100 MINA:
FILING PARE: 09.00.200
CLARSETFORTION: CURRENT ON CLARACTERION: CURRENT ON COMPANY.
 PRIOR PARLICATION MATCH AUTO-
APPLICATION WINBER, 09/06;743
FILING DATE, APPLI 21, 1998
ATCHRIY/AGENT INFORMATION:
REGISTRATION WINBER, 43, 168
REGISTRATION WINBER, 43, 168
TRECOMMUNICATION INFORMATION:
 MUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Genomics, Inc.
STREET: 310 Porter Drive
CITY: Palo Alto
 CLONE: 059953
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 Sequence 1, Application US/09590540 Patent No. 6410267 GENERAL INFORMATION:
 TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
 LENGTH: 375 amino acids
TYPE: amino acid
 Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
 APPLICANT: Bandman, Olga
 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS
 LIBRARY: LUNGNOT01
 TELEX: <Unknown>
 USA
 STATE: CA
 COUNTRY:
 US-09-590-540-1
 US-09-590-540-1
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 66 EGEVYCCKFHPNGST-LASAGFDRLILLMNVYGDCDNYATLK-GHSGAVMELHYNTDGSM 123
 70 AWSGGLDHQLKNHDLNTDQ--ENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRT 127
 124 LFSASTDKTVAVWDSETGERVKRLKGHTSFVNSCYPARRGPQLVCTGSDDGTGKLWDIRK 183
 184 KAAIQİFQNTYQVLAVİFNDTSDQIİSGGIDNDIKVWDL-----RQNKLTYTMRGH 234
 235 ADSVTGLSLSSEGSYLLSNAMDN-TVRVMDVRPFAPKE----RCVKIFQGNVHN-FEKNL 288
 128 PCNAGTFSQPEKV--YTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTR-- 183
 184 ----CIRAFPNKOGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNA 239
 240 I--SPHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASS- 296
 14 EDGISSUKFSPNTSQFLLVSSWDTSVRLYDVPA---NSMRLKYQHTGAVLDCAF-YDPTH 69
 Gaps
 ch 10.0%; Score 176.5; DB 3; Length 375; LB 3inlarity 25.8%; Pred. No. 81.50-11; 80; Conservative 51; Mismatches 142; Indels 37;
APPLICANT: Lal, Presti
APPLICANT: Gueglet, Karl J.
APPLICANT: Gueglet, Karl J.
APPLICANT: Gueglet, Mell C.
APPLICANT: Petersonn, Chandra
TITLE OF INVENTION: HUMAN OTPASS-ASSOCIATED PROTEINS
COMMERCENDENC ADDRESS:
COMMERCENDENC ADDRESS:
COMMERCENTION: PROTEINS
COMMERCENTION: PROTEINS
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COMMERCENTION: PROTEINS
COMMERCENT
 SYSTEM: DOS
FastSEQ for Windows Version 2.0
 PF-0508 US
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/063,743
 NAME: Cerrone, Michael C
REGISTRATION NOMBER: 39,132
REFERENCE, DOCKET NUMBER: PF-O
TELECOMMUNICATION INFORMATION:
TELEBHONE: 650-855-0555
TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
 3, Diskette
IBM Compatible
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
 STRANDEDNESS: single
 PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM:
 ---YMYENDD 303
 349 KRLYMGEFSE 358
 LUNGNOT01
 Query Match
Best Local Similarity
 OPERATING SYSTEM:
 linear
 Palo Alto
 CLASSIFICATION:
 IMMEDIATE SOURCE:
 LIBRARY: LUNG
CLONE: 059953
 94304
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 COMPUTER:
 SOFTWARE:
 TOPOLOGY:
 US-09-063-743-1
 STATE:
 Matches
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Gaps

us-10-084-700-2.rai

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63 AFYDPTHAM-SGGLDHQLKMHDLNTDQE-NLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
 62 OFSPYGYYFVSGGHDRVARLWATDHYOPLRIFAGHLADVNCTRFHPNSNYVATGSADRTV 121
 121 KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY 180
 122 RLWD------130
 181 QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI 240
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 241 SFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
 4 SNEFKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDC 62
 63
 3 ASELKILYGHSGPVYGASFSPDRN-YLLSSSEDGTVRLWSLQTFTCLVGYKGHNYPVWDT
 Gaps
 Indels 107;
 DB 4; Length 250;
 APPLICANT: Mochile Resen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: Mo-10. Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 255
CORRESPONDENCES. 255
 Query March 9.6%; Score 169.5; DB 4; Best Local Similarity 21.5%; Pred. No. 2.5e-10; Marches 69; Conservative 44; Mismatches 101;
 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/08/190,802A
FILING DATE: 01-FEB-1994
 FEATURE:
OTHER INFORMATION: TFIID WD40 repeat region
 8600-0139
 ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
 131 --- CVRIPTGHKG------
 PRIOR APPLICATION NUMBER: 09/291,170
PRIOR FILING DATE: 1999-04-13
 301 MODIEHPEDGIFIRQVIDAET 321
 201 MONTVRLWDA--IKAFEDLET 219
 Sequence 38, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT FILING DATE: 2000-11-28
 ATTORNEY AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 860
TELECOMMUNICATION INFORMATION:
 NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 250
 COMPUTER READABLE FORM:
 TYPE: PRT
ORGANISM: Homo sapiens
 94306-0850
 CLASSIFICATION:
 USA
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 US-08-190-802A-38
 US-09-724-884-12
 COUNTRY:
 STATE:
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289 LRCSWSPDGSKIAAGSADRFVYVWDTTSRRILYKLPGHAGSINEVAFHPDEPIIISASSD 348
 63 APYDPTHAM-SGGLDHQLKMHDLNTDQE-NLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
 :|||}
122 RLMD------130
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 62 QFSPYGYYFVSGGHDRVARLWAIDHYQPLRIFAGHLADVNCTRFHPNSNYVAIGSADRIV 121
 121 KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY 180
 131 --- CVŘÍFTGHKG------PIHSL 145
 241 SPHNIHNTFATGGSDGFVNIMDPFNKKRLCQPHRYPTSIASLAFSNDGTTLAIASSYMYE 300
 146 TFSPNGRFLATCATDGRVLLWDIGHGLMVGELKGHTDTVCSLRFSRDGEILASGS---- 200
 4 SNEFKLMOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDC 62
 3 ASELKILYGHSGPVYGASFSPDRN-YLLSSSEDGTVRLWSLQTFTCLVGYKGHNYPVMDT 61
 Query Match 9.6%; Score 169.5; DB 4; Length 250; Best Local Sámilarity 21.8%; Pred. No. 2.5e-0.1 Marches 69; Conservative 44; Mismarches 101; Indels 107; Gaps
 APPLICANT: Vale, Ronald D.
APPLICANT: Hartuan, James J.
APPLICANT: Hartuan, James J.
APPLICANT: Hartuan, James J.
APPLICANT: Hartuan, James J.
THIS OF INVERTORY Nasays for the Defection of Microtubule THIS OF INVERTORY Nasays (2007) Harbard CHERNICAN TOR TOWNERS TO THE OF THE PROPERTORY NASASS (2009) 1,170A
CHERNY FILING DATE: 1999-04-13
PRIOR PELIZATION DATE: 1999-04-14
PRIOR PELIZATION DATE: 1999-04-14
PRIOR PELIZATION DATE: 1999-04-14
PRIOR PELIZATION DATE: 1999-04-14
PRIOR PELIZATION DATE: 1999-04-14
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PRIOR PELIZATION DATE: 1999-04-14
PRIOR PELIZATION DATE: 1999-04-14
PRIOR PELIZATION DATE: 1999-04-14
PRIOR PELIZATION DATE: 1999-04-14
 Sequence 12, Splication US/09724884
Patent No. 6429304
APPLICANT: Vale, Romaid D.
APPLICANT: Vale, Romaid D.
APPLICANT: The Regents of the University of California PAPLICANT: The Regents of the University of California APPLICANT: The Regents of the University of California TITLE OF INVENTION: Despiyeerization Inhibitors CREE REGENERS: 18557-10051009
CREAST APPLICANTON NUMBER: US/09/724,884
 FEATURE:
; OTHER INFORMATION: TFIID WD40 repeat region
US-09-291-170A-12
 Sequence 12, Application US/09291170A Patent No. 6410687 GENERAL INFORMATION:
 MDNTVRLWDA--IKAFEDLET 219
 301 MDDTEHPEDGIFIROVIDAET 321
 297 ---YMYEMDD 303
 349 KRLÝMGĚFSE 358
 TYPE: PRT
ORGANISM: Homo sapiens
 US-09-291-170A-12
 US-09-724-884-12
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us-10-084-700-2.rai

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14;
 65 TDSRLLVSASQDGKLIIWDSYTTNKVHAIPIRSSWVMTCAYAPSGNYVAC----- 114
 73 GGLDHQLKMHDLNTDQENL----VGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRT 127
 128 PCNAGTES-QPEKYYTLSVSGD-RLIV-GTAGRRVLVWDLRNMGYVQQR----RESSLKYQ 181
 174 GQCTTTFTGHTGDVWSLSLAPDTRLFVSGACDASAKLWDVRE-GMCROTFTGHESDI--- 229
 182 TRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAIS 241
 230 -NAICFFPNGNAFATGSDDATCRLPDLRADQELMTYSH------DNI--ICGITSVS 277
 26 TSQFLLVSS------WD--TSVRLYDVPANS---MRLKYQHTGAVLDCAFYDPTHAWS 72
 Indels 51, Gaps
 242 FHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIAS 295
 278 FSKSGRLLLAGYDDFNCNVWDALKADRAGVLAGHDNRVSCLGVTDDGMAVATGS 331
 Length 340;
 Sequence 38, Application US/08473089
Patent No. 6442586
GENERAL HYPROMATION
PAPLICANT: Non-Dorit
APLICANT: Ron, Dorit
 9.6%; Score 169.5; DB 3;
24.8%; Pred. No. 4.1e-10;
trive 43; Mismatches 127;
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
 INDIVIDUAL ISOLATE: G-Beta 1 bovine, Fig. 21
 REFERENCE/DOCKET NUMBER: 2550-0025.22
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
 FILING DATE: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ATTORNEY AGENT INFORMATION:
NAME: WIRASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
 TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 38:
 (202) 887-1500
 340 amino acids
 Best Local Similarity 24.88
Matches 73; Conservative
 MOLECULE TYPE: protein
HYPOTHETICAL: NO
 COMPUTER READABLE FORM:
 unknown
 TOPOLOGY: unknown
 CITY: Washington
 20006-1812
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 ANTI-SENSE: NO
ORIGINAL SOURCE
 USA
 TELEPHONE:
 US-08-477-346-38
 US-08-473-089-38
 COUNTRY:
 LENGTH:
 Query Match
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 65 TDSRLLVSASQDGKLINDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVAC----- 114
 73 GGLDHQLKMHDLNTDQENL----VGTHDAPIRCVEYCPBVNVMVTGSWDQTVKLWDPRT 127
 128 PCNAGTES-QPEKUYTLSVSGD-RLIV-GTAGRRVLVWDLRNMGYVQQR---RESSLKYQ 181
 182 TRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAIS 241
 230 -NAICFFPNGNAFATGSDDATCRLFDLRADQELMTYSH-----DNI--ICGITSVS 277
 26 TSQFLLVSS-----WD--TSVRLYDVPANS---WRLKYQHTGAVLDCAFYDPTHAWS 72
 Gaps
 242 FHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIAS 295
 278 FSKSGRLLLAGYDDFNCNVMDALKADRAGVLAGHDNRVSCLGVTDDGMAVATGS 331
 51;
 DB 1; Length 340;
 Query Match

9.6%; Score 169.5; DB 1; Length 3
Best Local Similarity 24.8%; Pred. No. 4.18-10.1

Matches 73; Conservative 43; Mismatches 127; Indels
 Sequence 19, Application US/08477346
Peterne 19, Application US/08477346
GARBAL INFORMATON:
RALICANT: Monit Derit
APLICANT: Monit Derit
TITLE OF INVARIATION: Mo-40 - Derived Peptides and Uses
TITLE OF INVARIATION: Thereof
CONTRASPONDENCES: 266
CONTRASPONDENCES: 266
 SOFWARE. Patentin Release #1.0, Version #1.25
SOREMEN PRELIGHION DAY.
RPELICATION NUMBER: US/06/477,346
CLASSIFICATION: 514
 G-Beta 1 bovine, Fig. 21
 PATOR APPLICATION DATA:
RAPLICATION DATA:
RAPLICATION DATE:
RALING DATE:
RALING DATE:
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RALING DATE:
RALING DATE:
RALING DAT
 STREET: 2000 Pennsylvania Avenue, NW
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 Morrison & Foerster
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 PELECOMMUNICATION INFORMATION:
 LENGTH: 340 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 Floppy disk
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
US-08-190-802A-38
 Washington
 20006-1812
 ANTI-SENSE: NO
 USA
 ADDRESSEE:
 US-08-477-346-38
 COUNTRY:
 RESULT 10
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unknown

TOPOLOGY:

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65 TDSRLLVSASQDGKLIIMDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVAC----- 114
 73 GGLDHQLKMHDLNTDQENL----VGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLMDPRT 127
 128 PCNAGTFS-OPEKVYTLSVSGD-RLIV-GTAGRRVLVWDLRNMGYVQQR---RESSLKYQ 181
 174 GOOTITIFIGHTGDVMSLSLAPDIRLFVSGACDASAKIMDVRE-GMCRQTFTGHESDI--- 229
 230 -NAICFFPNGNAFATGSDDATCRLFDLRADQELMIYSH------DNI--ICGITSVS 277
 26 TSQFLLVSS-----WD--TSVRLYDVPANS---MRLKYQHTGAVLDCAFYDPTHAMS 72
 182 TRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAIS
 51; Gaps
 242 FHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAPSNDGTTLAIAS 295
 278 FSKSGRLLLAGYDDFNCNVWDALKADRAGVLAGHDNRVSCLGVTDDGWAVATGS 331
 Ouery Match
9.6%; Score 169.5; DB 4; Length 340;
Best Local Similarity 24.8%; Predi No. 4,1-10;
Matches 73; Conservative 43; Mismatches 127; Indels 51;
Matches 73; Conservative 43; Mismatches 127; Indels 51;
 APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorif
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
OVERSONDENCES: 265
OVERSONDENCE APPRESS;
ADDRESSER: Morrison & Poorster
 Patentin Release #1.0, Version #1.25
 ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G-Beta 1 bovine, Fig. 21
 3: Morrison & Foerster
2000 Pennsylvania Avenue, NW
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
 Sequence 38, Application US/08487072A
Patent No. 6423684
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ATTORNEY AGENT INC.
ATTORNEY AGENT WARE HOUSE MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2:
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 887-1500
 TELEFAX: (202) 897-0763
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
 ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
 340 amino acids
 TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 Washington
 amino acid
 GENERAL INFORMATION:
 CLASSIFICATION:
 ANTI-SENSE: NO
 USA
 US-08-487-072A-38
 US-08-473-089-38
 COUNTRY:
 STREET;
 LENGTH
 RESULT 12
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APPLICANT: Liveage. Strinvas R.V.
APPLICANT: Menn of certain a Strinvas R.V.
APPLICANT: Chen Yikang
APPLICANT: Chen Yikang
APPLICANT: Buck Ritachein, Havel
TITLE OF INVENTION: PEPTIDSS AND OTHER SMALL WOLKCULSS DERIVED FROM REGIONS
TITLE OF INVENTION: OF INTERACTING PROTEINS AND USES THEREOF
 65 TDSRLLVSASQDGKLJIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVAC----- 114
 73 GGLOHQLKOMHDLNTDQENL----VGTHDAPIRCVEXCPEVNVWTGSWDQTVKLMDPRT 127
 115 GGLDNICSIYNLKTREGNVRVSRELAGHTGYLSCCRPLDD-NQIVTSSGDTTCALWDIET 173
 128 PCNAGIFS-QPEKVYTLSVSGD-RLIV-GTAGRRVLVWDLRNMGYVQQR----RESSLKYQ 181
 182 TRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAIS 241
 230 -NAICFFPNGNAFATGSDDATCRLFDLRADQELMTYSH------DNI--ICGITSVS 277
 72
 65 TDSRLLVSASQDGKLIIMDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVAC----- 114
 73 GGLDHQLKMHDLNTDQENL----VGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRT 127
 128 PCNAGTES-QPEKVYTLSVSGD-RLIV-GTAGRRVLVMDLRNMGYVQQR---RESSLKYQ 181
 174 GQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVRE-GWCRQTFTGHESDI--- 229
 182 TRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAIS 241
 26 TSQFLLVSS-----WD--TSVRLYDVPANS---MRLKYQHTGAVLDCAFYDPTHAMS 72
 26 TSQFLLVSS-----WD--TSVRLYDVPANS---MRLKYQHTGAVLDCAFYDPTHAWS
 Indels 51; Gaps
 242 FHNIHNTFATGGSDGFVNIWDPFNKKRLCOFHRYPTSIASLAFSNDGTTLAIAS 295
 278 FSKSGRLLLAGYDDFNCNVWDALKADRAGVLAGHDNRVSCLGVTDDGMAVATGS 331
 Indels 51;
 Length 340;
 Length 340;
 DB 4;
 1 Similarity 24.8%; Pred. No. 4.1e-10; 73; Conservative 43; Mismatches 127;
 9.6%; Score 169.5; DB 4;
24.8%; Pred. No. 4.1e-10;
tive 43; Mismatches 127;
 G-Beta 1 bovine, Fig. 21
 9.6%; Score 169.5;
24.8%; Pred. No. 4.1
 FILE REFERENCE: 6923-074
CURRENT APPLICATION WUMBER: US/09/245,039
CURRENT FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 10
 Sequence 1, Application US/09245039
Patent No. 655552
GENERAL INFORMATION:
 Patentin Ver. 2.0
 73; Conservative
MOLECULE TYPE: protein HYPOTHETICAL: NO
 ORIGINAL SOURCE;
INDIVIDUAL ISOLATE:
US-08-487-072A-38
 ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 73; Conserv
 Best Local Similarity
Matches 73; Conserv
 ANTI-SENSE: NO
 340
 US-09-245-039-1
 US-09-245-039-1
 SOFTWARE: F
 TYPE: PRT
 Query Match
 LENGTH:
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us-10-084-700-2.rai

| 230 -NATCEPENNARATGSDARCE (FILES OF SWEET)                                                                      | :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |     |
|-----------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| 7 242 PHNIHNTPATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASIAFSNUGTTIAIAS 295                                                | 241 SFHNIHNTPATGGSDGFVNIMDFNN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 300 |
| 278 FSKSGRLILAGYDDFNCNYWDALKADRAGVLAGHDNRVSCLGVTDDGMAVATGS 331                                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 634 |
| SSULT 14                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |
|                                                                                                                 | Db 635 MDNTVRLMDAIKAFEDLET 653                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
| GENERAL INFORMATION:<br>APPLICANT: Tjian, Robert                                                                | RESULT 15<br>US-08-646-715-18                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |     |
| APPLICANT: Comai, Lucio<br>APPLICANT: Dynlact, Brian D.                                                         | ; Sequence 18, Application US/08646715<br>; Patent No. 5637686                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
| APPLICANT: Hoey, Timothy APPLICANT: Ruppert, Slegfried                                                          | ; GENERAL INFORMATION:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |     |
| APPLICANT: Tanese, Naoko<br>APPLICANT: Wang, Edith                                                              | APPLICANT: Comai, Lucio                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |     |
| APPLICANT: Weinzierl, Robert O.J. TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,                  | APPLICANT: Hoey, Timothy ; APPLICANT: Rubbert Steefried                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |     |
| TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAPS AND METHODS OF USE NUMBER OF SEQUENCES: 36                      | APPLICANT: Tanese, Naoko                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |
| CORRESPONDENCE ADDRESS: ADDRESSEE: FLEHR, HORBACH, TEST, ALBRITTON & HERBERT CTBERT, A PERHACAGARY CARLAR SALON | , APPLICANT: Weinzierl, Robert O.J. ; TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |     |
| CITY: San Francisco<br>STATE: California                                                                        | ITILE OF INVENTION: NUCLEIC ACIDS ENCODING TARS AND METHODS OF US                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |     |
| COUNTRY: USA                                                                                                    | CORRESPONDENCE ADDRESS: ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |     |
| COMPUTER READARLE FORM:                                                                                         | ; STREET: 4 Embarcadero Center, Suite 3400<br>; CITY: San Francisco                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |     |
| MELLUM TYPE: Floppy disk<br>COMPUTER: IBM PC compatible                                                         | ; STATE: California<br>; COUNTRY: USA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |     |
| OPERATING SYSTEM: PC-DOS/MS-DOS<br>SOFTWARE: Patentin Release #1.0, Version #1.25                               | ; ZIP: 94111-4187<br>; COMPUTER READABLE FORM:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
| CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/188,582                                                     | MBDIUM TYPE: Floppy disk                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |
| FILING DATE: 28-JAN-1994<br>CLASSIFICATION: 435                                                                 | OPERATING SYSTEM: PC-DOS/MS-DOS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |     |
| ATTORNEY/AGENT INFORMATION; NAME: Osman, Richard A                                                              | CURRENT APPLICATION DATA:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     |
| RECISTRATION WIMBER: 36,627<br>REPERRICE/DOCKET WIMBER: A-57650-2/ATT/PAG                                       | FILING DATE: 09-MAY-1996                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |     |
| TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989                                                        | PRIOR APPLICATION DATA:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |     |
| TELERAX: (415) 398-3249                                                                                         | # APPLICATION NUMBER: US 08/188,582   FILING DATE: 28-JAN-1994                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
| INFORMATION FOR SEC ID NO: 18:                                                                                  | ; ATTORNEY/AGENT INFORMATION:<br>; NAME: Osman, Richard A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     |
| LENGTH: 704 amino acids                                                                                         | ; REGISTRATION NUMBER: 36,627<br>; REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |     |
| TOPOLOGY: linear<br>MOLBCULE TYPE: protein                                                                      | TELECOMUNICATION INFORMATION:<br>  TELEPHONE (415) 781-1989<br>  TELEPHONE (715) 200 2000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     |
| -08-188-582-18                                                                                                  | ; TELEKA: 112) 398-3249                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |     |
| Query Match 9.6%; Score 169.5; DB 1; Length 704; Best Local Similarity 21.5%; Pred No. 1.30-ng.                 | SEQUENCE CHARACTERISTICS:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |     |
| Matches 69; Conservative 44; Mismatches 101; Indels 107; Gaps 9;                                                | ; LENGTH: 704 amino acids ; TYPE: amino acid                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |     |
| 4 SNBPKLNQPPEDGISSVKPSPYTSQPLLVSSWDTSVRLYDVPANSMELKYQ-HTGAVLDC 62<br>11   1   1   1   1   1   1   1   1   4   4 | ; TOPOLCOY: linear;<br>; MOLECULE TYPE: protein<br>US-08-646-712-12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |     |
| 63 APYDPTHAM-SOGLDHOLKKHDLINTDQB-NLVGTHDAPIRCVEYCTEVKVMVTGSWDQTV 120                                            | tch<br>al Similarity 21.5%; Score 169.5; DB 1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |     |
| 496 QFSPYGYYFVSGGHDRVARLMATDHYQPLRIFAGHLADVNCTRFHPNSNYVATGSADRTV 555                                            | Matches                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ,6  |
| TAGRRVLVWDLRNMGYVQQRRESSLKY                                                                                     | 4 SNEPKLAQPPEDGISSUKFSPNTSQFILVSSWDTSVRLYDVPANSNRLKYQ-HTGAVIDC 62     437 ASELKILYGHSGPVYQAFSSPDN-YIJSSSRDVOTVURKSICTOPTF-TIAVYCHAVDATA-06                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 62  |
| 556 KLMD 564                                                                                                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | n ( |
| 181 ÇTRCIRAFPNKÇGYVLSSIEGRVAVEYLDPSPEVÇKKKYAFKCHRLKENNIEÇIYPVNAI 240                                            | ST ALL STREET SOCIED TO THE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET ST | 120 |

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OM protein . protein search, using sw model Run on:

November 12, 2003, 20:08:53; Search time 30 Seconds
(vithour alignments)
(077.792 Million cell updates/sec

1 MTGSNEFKLNQPPEDGISSV........328 US-10-084-700-2 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

644079 segs, 171749292 residues Searched:

Total number of hits satisfying chosen parameters;

644079

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications And Andrea (1997) Published Applications Andrea (1997) Published Applications Andrea (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published (1997) Published Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

STIMMARIES

|            | Description              | Sequence 4. Appli | Segmence 2. Appli | •                  |                  |                  |                  |                  | Semience 30. Appl | Seguence 712. App |                  |                   | Semience 1045, An  | Semience 1045 An   | Semience 11 April | · Sequence 1, Appli |
|------------|--------------------------|-------------------|-------------------|--------------------|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|-------------------|--------------------|--------------------|-------------------|---------------------|
| SOUTHWITES | DI OI                    | US-09-095-881-4   | US-10-084-700-2   | US-09-925-301-1301 | US-10-084-700-27 | US-10-084-700-29 | US-10-084-700-32 | US-10-084-700-31 | US-10-084-700-30  | US-09-925-302-712 | US-10-084-700-28 | US-09-903-190-157 | US-09-925-299-1045 | US-09-925-299-1045 | US-10-077-111-11  | US-10-119-932-1     |
|            | 80                       | 1 27              | 14                | φ                  | 14               | 14               | 14               | 14               | 14                | 6                 | 14               | 12                | Ø                  | 17                 | 14                | 14                  |
|            | Query<br>Match Length DB | 328               | 328               | 332                | 330              | 326              | 365              | 352              | 368               | 413               | 341              | 29                | 100                | 100                | 742               | 375                 |
| æ          | Query                    | 100.0             | 100.0             | 100.0              | 98.6             | 98.4             | 30.4             | 28.9             | 28.7              | 28.7              | 20.1             | 14.6              | 11.1               | 11.1               | 11.1              | 10.0                |
|            | Score                    | 1772              | 1772              | 1772               | 1747             | 1743             | 538              | 511.5            | 509               | 509               | 356              | 258               | 197.5              | 197.5              | 197.5             | 176.5               |
|            | Result<br>No.            | -                 | 8                 | m                  | 4                | 'n               | 9                | 4                | 80                | 6                 | 10               | 11                | 12                 | 13                 | 14                | 15                  |

| Sequence 10, Appl | 'n              | Sequence 2, Appli | 4               | 50,              | ۲,              | 2                | 7                | 2                 | 14               | ý,              | 9                | S,              | S                | 8               | 6               | 6                | 8               | 8                | 18               | 4,              | 4                | 21               | 21                | 'n              | 'n               | 6               | 27               | 23     | Sequence 25, Appl |
|-------------------|-----------------|-------------------|-----------------|------------------|-----------------|------------------|------------------|-------------------|------------------|-----------------|------------------|-----------------|------------------|-----------------|-----------------|------------------|-----------------|------------------|------------------|-----------------|------------------|------------------|-------------------|-----------------|------------------|-----------------|------------------|--------|-------------------|
| US-10-077-111-10  | US-10-274-525-3 | US-09-226-248B-2  | US-10-320-778-1 | US-10-245-618-20 | US-09-213-888-7 | US-09-213-888-10 | US-09-328-877A-7 | US-09-328-877A-10 | US-10-245-618-14 | US-09-213-888-6 | US-09-328-877A-6 | US-09-213-888-5 | US-09-328-877A-5 | US-10-245-618-8 | US-09-213-888-9 | US-09-328-877A-9 | US-09-213-888-8 | US-09-328-877A-8 | US-10-245-618-18 | US-09-213-888-4 | US-09-328-877A-4 | US-09-213-888-21 | US-09-328-877A-21 | US-09-213-888-3 | US-09-328-877A-3 | US-10-245-618-6 | US-09-213-888-27 | 9-328- | US-09-213-888-25  |
| 7,4               | 12              | 10                | 12              | 12               | 10              | 2                | 2                | 10                | 12               | ទ               | 2                |                 |                  | 12              |                 |                  | 9               | 10               | 12               | 2               | 10               | 10               | 9                 | ន               | 10               | 12              | ទ                | 2      | 2                 |
| 1356              | 486             | 340               | 340             | 281              | 540             | 540              | 540              | 540               | 540              | 545             | 545              | 553             | 553              | 553             | 559             | 559              | 589             | 289              | 289              | 292             | 265              | 626              | 626               | 627             | 627              | 627             | 999              | 999    | 699               |
| 6.6               | 6.6             | 9.6               | 9.6             | 4.6              | 9.4             | 9.4              | 9.4              | 9.4               | 9.4              | 9.4             | 9.4              | 9.4             | 9.4              | 9.4             | 9.4             | 9.4              | 9.4             | 9.4              | 4.               | 4.              | 4.               | 9.4              | 4.                | 9.4             | 4.6              | 9.4             | 4.6              | 9.6    | 9.4               |
| 176               | 175.5           | 169.5             | 169.5           | 166.5            | 166.5           | 166.5            | 166.5            | 166.5             | 166.5            | 166.5           | 166.5            | 166.5           | 166.5            | 166.5           | 166.5           | 166.5            | 166.5           | 166.5            | 166.5            | 166.5           | 166.5            | 166.5            | 166.5             | 166.5           | 166.5            | 166.5           | 166.5            | 166.5  | 166.5             |
| 16                | 17              | 18                | 13              | 50               | 21              | 22               | 23               | 24                | 25               | 56              | 27               | 58              | 53               | 30              | 31              | 35               | 33              | 34               | 35               | 36              | 37               | 38               | 33                | 40              | 41               | 43              | 43               | 44     | 45                |

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|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------|
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                             | 9                                                            |                                                              |                                                                  |                                                               |                                                              |                                                              |                                                              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Gaps                                                        | AS                                                           | SAV                                                          | 8=5                                                              | SLK)                                                          | ;                                                            | ¥.                                                           | Z¥.                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                             | 岳二                                                           | GH3                                                          | MSE -                                                            | SES:                                                          | ESS S                                                        | Z Z                                                          | . YP                                                         |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 28;                                                         | ž=                                                           | ĽŽ.                                                          | ¥=\$                                                             | SOR!                                                          | =8                                                           | 150                                                          | - G                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | я<br>                                                       | ISMR                                                         | SMR                                                          | 3                                                                | 2.5                                                           | =₹                                                           | ENN                                                          | ES.                                                          |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Length 328;<br>Indels 0;                                    | APA .                                                        | /PA                                                          | CPE                                                              | RNA                                                           | =                                                            | RLK                                                          | ੜ                                                            |
| THE WILD-TYPE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1-4                                                         | MTGSNEFKINOPPEDGISSVKFSPNTSQF1LVSSWDTSVRLYDVPANSMRLKYQHTGAVL | mtgsnefklmoppedgissvkfspntsofllvsswdtsvrlydvpansmrlkychtgavl | DCAFYDPTHAMSGGLDHQLKMHDLMTDQRNLVGFHDAPTRCVFYCPEYNYMYTGSWDQTV<br> | KLWDPRTPCNAGTESQPEKVYTLSVSGDR.LIVGTAGRRVLVWDLRNMGYVQQRRESSLKY | KLWDPRIPCNAGIPSQPEKVYTLSVSGDRLIVGIAGRRVLVWDLRNMGYVQQRRESSLKY | QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI | QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI |
| T-Q                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | DB 10,<br>180,<br>0,                                        | SVR<br>                                                      | SVR                                                          | AL L                                                             | RVL                                                           | = <u>`</u>                                                   | KXA                                                          | K¥=                                                          |
| MI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Score 1772; DB 1<br>Pred. No. 6e-180;<br>Mismatches 0       | Z Z                                                          | MD                                                           | 9=9                                                              | AGR                                                           | =8                                                           | ÖK.                                                          | -Š                                                           |
| THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 6e<br>hes                                                   | TAS:                                                         | LVS                                                          | 3=3                                                              | 200                                                           |                                                              | SPE                                                          | SPE                                                          |
| -4 Application US/09058811 US20020131040231 ORMATION 0 DESCRIPTION OF LOSS OF WINSWILDN: DEBCE: 1405.003 , 200130, 437 LING APRE: 1998-06-11 LING APRE: 1998-06-11 EXECT DESCRIPTION OF LOSS OF WINGWILDN: 198-06-11 LING APRE: 1998-06-11 Fast:SEC For Windows Version 3.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Score 1772;<br>Pred. No. 6e<br>Mismatches                   | <u> </u>                                                     | P.                                                           | OEN<br>CEN                                                       | DRL                                                           | = 12                                                         | TOP                                                          | -6                                                           |
| on 15/09095881 00421 00421 DETECTION OF LOSS OF MARBUR GRNE .003 .7 200130,495,891 198 06-11 198 06-11 198 06-12 vr Windows Version 3.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ore<br>dism                                                 | STYS                                                         | SING                                                         | 2 - 2                                                            | 3vsg                                                          |                                                              | VEV.                                                         | VEZ                                                          |
| 09095881<br>TON OF LOSS<br>GENE<br>1200130-437<br>1200130-437<br>1200130-437<br>1200130-437                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | S.<br>Pre                                                   | KPS!                                                         | KFSI                                                         |                                                                  | Y                                                             |                                                              | 3RV                                                          | 38                                                           |
| 100 01 CENE 2001: US/6-11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |                                                             | SS.                                                          | SSV                                                          |                                                                  | BKV                                                           | =\$                                                          | SIE                                                          | SIE<br>SIE                                                   |
| S/09<br>CTIC<br>ER:<br>BB1<br>Odov                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 100.0%;<br>100.0%;<br>ive                                   | 15G                                                          | EDG1                                                         |                                                                  | 408                                                           | - S                                                          | VIS.                                                         | -SE                                                          |
| ion US/( 3042A1 Toda Toda Deffect huBUB1 FS.003 / FUNBER: 1998-C S: 15 or Winde                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 100<br>larity 100<br>Conservative                           | IAG I                                                        | I O                                                          | 88—88<br>—88<br>—88                                              | GT.                                                           | _5                                                           | 8                                                            | - <u>8</u>                                                   |
| cation<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colision<br>colis | ë Ç                                                         | 3=                                                           | Ē                                                            | HE H                                                             | Ď.                                                            | = <u>8</u>                                                   | FPN                                                          | -64<br>-67                                                   |
| SEO PAICS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | lari                                                        | SNE                                                          | SNE                                                          |                                                                  | PRT                                                           | PRT                                                          | I.R.                                                         | ZA.                                                          |
| Application US/0905881<br>USZOZO12342A1<br>USZOZO1234A2A<br>SSEAFY, TOGM<br>WINEWATUON DETECTION OF L<br>WINEWATUON DETECTION OF L<br>WINEWATUON DETECTION OF L<br>WINEWATUON INBURSE USYO<br>PELICATION NUMBER: USYO<br>SECTION NOWER: 198-06-11<br>SECTION NOWER: 198-06-11<br>SECTION NOWER: 198-06-11<br>FRESEED FOR WINDOWS VEYS<br>188-189-189-189-189-189-189-189-189-189-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | imi,                                                        | E C                                                          | MIG                                                          | <u>8</u> —8                                                      | KLW                                                           | - P                                                          | OTE<br>1                                                     | Z                                                            |
| 1981-<br>TINFO<br>TINFO<br>TERRE<br>PEREN<br>PEREN<br>132<br>132<br>133<br>131-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ch<br>11 Sim<br>328,                                        | т.                                                           | - ;                                                          | 61                                                               | 121                                                           | 121                                                          | 181                                                          | 181                                                          |
| 19-095-881-4 19-096-881-4 19-096-881-4 19-096-881-4 19-096-881-4 19-096-881-4 19-096-881-4 19-096-881-4 19-096-881-4 19-096-881-4 19-096-881-4 19-096-881-4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Mat                                                         |                                                              |                                                              |                                                                  | н                                                             | -                                                            | -                                                            | -                                                            |
| REBULT.  1867-05-681-4  1867-061-681-4  1867-061-681-4  1867-061-681-681-681-681-681-681-681-681-681-6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Query Match<br>Best Local Similarity<br>Matches 328, Conser |                                                              |                                                              |                                                                  |                                                               |                                                              |                                                              |                                                              |
| SEGURAL SERVIT I SEGURACE 4, A SECURACE 4, A SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE 10 SECURACE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | S # 2                                                       | à                                                            | g 2                                                          | <u> </u>                                                         | à                                                             | ą                                                            | à                                                            | 윰                                                            |
| _                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                             | -                                                            | - '                                                          |                                                                  | •                                                             | -                                                            | ~                                                            | _                                                            |

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 61 DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
 121 KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY 180
 240
 241 SFRINIHWIPATGGSOGPNYIMDPPNKKALOQPHRYPTSIASIAFSNDGTTLAIASSYMTE 300
245 SFRINIHWIPATGASOGPNYIMDPPNKKALOQPHRYPTSIASIAFSNDGTTLAIASSYMTE 304
245 SFRINIHVRATGASOGFNYIMDPPNKKALOQPHRYPSIASIAFSNDGTTLAIASSYMTE 304
 124
 184
 244
 9
 64
 61 DCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
 61 DCAFYDPTHAWSGGLDHQLAMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
 121 KLWDPRIPCNAGIPSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNWCYVQQRRESSLKY 180
 180
 9
 5 MIGSNEFKLNQPPEDGISSVRFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL
 65 DCAFYDPTHAMSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCEVONVMVTGSWDQTV
 125 KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY
 1 MTGSNEFKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL
 181 QTRCIRAFPUKQGYVLSSIEGRVAVEYLDPSPBVQKKKYAFKCHRLKENNIEQIYPVNAI
 1 MTGSNEFKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL
 Gaps
 121 KLWDPRTPCNAGTFSQPEKVYTLSVSGBRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY
 Gaps
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 Length 332;
 Length 330;
 Indels
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 APPLICANTA Seeiey. Tood
TITLE OF INVENTION: had 62 by 18 your CANCERS
FILE REFERENCE: PF.0.146 0.04.700130, 41801
FILE REFERENCE: PF.0.146 0.04.700130, 41801
CURRENT APPLICATION WOMERS: 0.06.700
CURRENT FILING DATE: 2002-02.27
SOFTWARE: FASTS OF WINDOWS VERSION 4.0
 Ouery Match 100.0%; Score 1772; DB 9; Best Local Similarity 100.0%; Pred. No. 6.1e-180; Matches 328; Conservative 0; Mismatches 0;
 Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-177,
Matches 324; Conservative 0; Mismatches 0;
 305 MDDTEHPEDGIFIRQVIDAETKPKSPCT 332
 301 MDDTEHPEDGIFIRQVTDAETKPKSPCT 328
 ; Sequence 27, Application US/10084700
; Publication No. US20020160403A1
; GENERAL INFORMATION:
 ; SEQ ID NO 27
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-084-700-27
 LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
 US-09-925-301-1301
SEQ ID NO 1301
 US-10-084-700-27
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 241 SFHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
 180
 SFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
 61 DCAFYDPTHAMSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTV 120
 61 DCAFYDPTHAMSGGLDHQLKMHDLNTDQBNLVGTHDAPIRCVEYCPEVNVMYTGSWDQTV 120
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 241 SFHNIHNTFATGGSDGFVNIWDPFNKKRLCOFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
 241 SFHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSYMYE 300
 9
 CTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI
 1 MTGSNEFKLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYBVPANSMRLKYQHTGAVL
 KLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY
 Gaps
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 DB 14; Length 328;
 Sequence 1010 Lapplication US/09925301
Patents No. 10520020041.
GrankEAL INFORMATION: 10.
GrankEAL INFORMATION: 10.
TITLE OF INFORTION: Nucleic Acids, Proteins and Antibodise FILE REPERBYCE: PAIGS.
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10.
PRIOR PAILNG DATE: 2001-08-10.
PRIOR PILING DATE: 5000-03-08
PRIOR PILING DATE: 5000-03-08
PRIOR FILING DATE: 5000-03-08
PRIOR PILING DATE: 50000-03-08
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 tch 100.0%; Score 1772; DB 14; al Similarity 100.0%; Pred. No. 6e-180; 328; Conservative 0; Mismatches 0;
 301 MODTEHPEDGIFIRQVTDAETKPKSPCT 328
 301 MDDTEHPEDGIFIRQVTDAETKPKSPCT 328
 301 MDDTEHPEDGIFIRQVTDAETKPKSPCT 328
 301 MDDTEHPEDGIFIRQVTDAETKPKSPCT 328
 , ORGANISM: Homo sapien
US-10-084-700-2
 US-09-925-301-1301
 SEQ ID NO 2
LENGTH: 328
 TYPE: PRT
 Query Match
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229 NNIEQIYPVNAISFHNIHNTFATGGSDGFVNIWDPPNKKRLCQFHRYPTSIASL---AFS 285
 264 NGQSLVYPVNSIAFHDLYGTFVTAGGDGTFNFWDKNQRHRL---KGYPTLQASIPVCSFN 320
 63 AFY--DPTHAWSGGLDHQLKMHDLANTDQENLVGTHDARIRCVEY--CPEVNV--MVTGSW 116
 146 DKTIKYMDMRQPQPVSTVVMMPERVYSMDNKQSLLVVATAERHJAIINLANPTTIFKATTS 205
 177 SLKYQTRÇIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKK-YAFKCHRLK-----E 228
 63 AF-YDPTHAWSGGLDHQLKOHDLNTDQENLVGTHDAPIRCVEYCPEVN----VMVTGSWDQ 118
 119 TVKLWDPRTPCNAGTESQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSL 178
 179 KYOTRCIRAPPNKOGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVN 238
 239 AISFHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASSY- 297
 259 SIAPHPQYGTFSTAGSDGTFSFWDKDSHQRLKSYPNVGGTISCSTFNRTGDIFAXAISYD 318
 14. TLKYWDLRQSTPIATVSLPERVYAMDCVHPLLTVATAERNICVINLSEPTKIFKLAMSPL 200
 6 EFKLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSM---RLKYQHTGAVLDC 62
 4 SNEFKLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQH-TGAVLDC
 26 ANDIVINSPAEDSISDIAFSPQQDFMFSASSWDGKVRIWDVQNGVPQGRACHESSSPVLC
 86 TRWSNDGTKVASGGCDNALKLYDIASGQTQQIGMHSAPIKVLRFVQCGPSNTECIVTGSW
 117 DQTVKLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRES
 22 DVEVAQPPEDSISDLAFSPQ-AEYLAASSWDSKVRIYEVQATGQSIGKALYEHQGPVLSV
 201 FFQTRSLACFIKGDGYAIGSVEGRCAIQNIDERDASQ--NFSFRCHRNQAGNSADVYSVN
 Query Match

Query Match

Best Local Similarity 34.8%; Pred. No. 1.16-45;

Marches 115; Conservative 58; Mismarches 147; Indels 15;

Marches 115; Conservative 58; Mismarches 147; Indels 15;
 Length 365;
 Ouery Match 30.4%, Score 538; DB 14; Length 3 Best Local Similarity 35.7%, Pred. No. 1.7e-48; Matches 122; Conservative 59, Mismatches 135; Indels Matches 125, Conservative 59, Mismatches 135; Indels
 Sequence J. Application U8/100e4100.
Publication U8/100e4100.
Publication U8/100e4100.
Publication U8/100e4100.
THE CONTROL Sealer, Frod Control Contr
 286 NDGTTLAIASSYMY---EMDDTEHPEDGIFIRQVTDAETKPK 324
 321 RNGSVFAYALSYDWHQGHMGNRPDYPNVIRLHATTDEEVKEK 362
 298 --- MYEMDDIEHPEDGIFIRQVIDAETKPK 324
 ORGANISM: Schizosaccharomyces pombe
 US-10-084-700-31
 US-10-084-700-31
 LENGTH: 352
TYPE: PRT
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241 SFHNIHNFRATGGSDGFWINDPPWKRLQPHRYPTSIASLAFSNDGTTLAIASSYMTE 300
241 SFHNIHNFRATGGSDGFWINDPBWKRLQPHRYPTSIASLAFSNDGTTLAIASSYMTE 300
242 SFHNIHNFRATGGSDGFWINDPBWKRLQPHRYPTSIASLAFSNDGTTLAIASSYMTE 300
 61 DCAFYDPTHAWSGGLDHQLKMHDLMTDQBNLVGTHDAPIRCVEYCPEVUVWVTGSWDGTV 120
 61 DCAFYDFTHAWSGLDHQLNYHDLNYDQENLVGTHDAPIRCVEYCPEVNYNYTGSWDGTV 120
 12. KLMDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESSLKY 180
 QTRCIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAI 240
 241 SPHNIHNTEATGSDGFWINDPRWKRLCOFHRYTSIASIAFSNDGTTLAIASSWWE 300
241 SPHNIHNTEATGGSDGFWINDPPWKRALQOFHRYPSIASIAFSNDGTTLAIASSWWE 300
241 SPHNIHNTEATGGSDGFWINDPPWKRALQOFHRYPSIASIAFSNDGTTLAIASSWWE 300
 9
 1 MTGSNEPKLNQPPEDGISSVKFSPNTSQPLLVSSNDTSVRLYDVPANSMRLKYQHTGAVL 60
 1 MTGSNEPKLNQPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVL
 Gaps
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 Length 326,
 US-10-064-700-22
US-10-064-700-22
PADICATE 10 NO USZ0020160403A1
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PADILOWHY 208-04-7
PATEL 064 NOWANTOW HORDAS GENE INVOLVED IN HUMAN CANCERS
PATEL 064 NOWANTOW HUMBER 105/10/044,700
UNRABEN PATELNG UN UNDARS 130/10/044,700
WARREN PATELNG UN NOS: 32
PORTWARN PATELNG UN NOS: 32
PROFUNANCY SASTERQ COT WINDOWS VERSION 4.0
 Indels
 APPLICANT: SeeLey, Todd
TITLE OF INVENTION: habus GRNE INVOLVED IN HUWAN CANCERS
TELE REPERRENE. FP 0-106.004/200130.438DJ
CURRENT APPLICATION WINNERS. 106/1064,700
NUMBER OF SEQ ID NOS: 22
SOFTWARE PEASEED for windows Version 4.0
SEQ ID NO. 29
 Query Match
98.4%; Score 1743; DB 14;
Best Local Similarity 99.7%; Pred. No. 7.2e-177;
Matches 324; Conservative 0; Mismatches 1;
 MDDTEHPEDGIFIRQVTDAETKPKS 325
 301 MDDTEHPEDGIFIRQVIDAETKPKS 325
 MODTEHPEDGIFIRQVIDAETKPK 324
 301 MDDTEHPEDGIFIROVTDAETKPK 324
 Sequence 29, Application US/10084700 Publication No. US20020160403A1 GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-084-700-32
 , ORGANISM: Mus musculus
US-10-084-700-29
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177
 76 DIEVTSSPODSIGCLSFSPPTLPGNFLIAGSWANDVRCWEVQDSGQTIPKAQQMHTGPVL 135
 D-CAFYDPTHAWSGGLDHQLKMHDLNTDQSNLVGTHDAPIRCVEY--CPEVNVMVTGSWD 117
 178 LKYQTRCIRAFPNKQ----GYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNI-- 231
 232 -EQIYPVNAISPHNIHNTFATGGSDGFVNIMDPFNKKRLCQFHRYPTSIASLAFSNDGTT 290
 374 SODIYAVNGIAFHPVHGTLATVGSDGRFSFWDKDARTKLKTSEQLDQPISACCFNHNGNI 374
 9
 CARYDPTHAWSGLDHQLKMHDLNTDQENLVGTHDAPIRCVEYC.....PEVNV- 110
 111 ------MVTGSWDQTVKLWDPRT-----PCNAGTFSQPEKVYTLSVSGDRL 150
 104 ICRICKYGDDKLIAASHDGLIEVIDPRNYGDGVIAVKNINSNNTKVKNKIFTMDTNSSRL 163
 8 KLNOPPEDGISSVKFSPNTSQFLLVSSWDTSVRLY--DVPANSM----RLKYQHTGAVLD 61
 5 QIBQAPKDYISDIKIIPSKS-LELITS#DGSLTVYKFDIQAKNVDLLQSLRYKH--PLLC 61
 62 CNFID-------NTDLQIYVGTVQGEILKVDLIGSPSFQALTNNEANLG 103
 151 IVGTAGRRVLVWDL----RNMGYVQQRRESSLKYQTRCIRAFPNKQ-GYVLSSIEGRVAV 205
 206 EYLDPSPE--VQKKKYAFKCHRLKENNIEQIYPVNALSFHNIHNTFATGGSDGFVNIMDP 263
 6 BFKLNQPPEDGISSVKPSPNT--SQFLLVSSWDTSVRLYDVPANSM---RLKYQHTGAVL
 118 QTVKLWDPRTPCNAGTFSQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESS
 Gaps
 Query March 20.1%; Score 36; DB 14; Length 341; Best Local Siniarity 30.1% Pred. No. 3.7e-29; Indels 76; Gaps Matches 109; Conservative 57; Mismatches 106; Indels 76; Gaps
 20;
 Query Match

28.7%; Score 509; DB 9; Length 413;
Best Local Similarity 34.3%; Precd. No. 2.5e-45.

Matches 116; Conservative 61; Mismatches 141; Indels :
 Sequence 2. A APPLICATION US/10084700
Publication No. 185002016040381
Publication No. 185002016040381
Publication No. 185002016040381
TILE BERSENER: PPO 4046 0.04/700110 43801
CURRENT APPLICATION NOMERS: 05/10/084,700
NUMBER OF SEQ ID NOS: 32
SOFTWARE PERSEDE FOR Windows Version 4.0
SED IN 78
 264 FNKKRLCQFHRY-PTSIASLAFSNDGTTLAIASSYMYEMDDT 304
 291 LAIASSYMYEMDD---TEHPEDGIFIRQVTDAETKPKS 325
 375 FAYASSYDWSKGHEFYNPOKKNYIFLRNAAE-ELKPRN 411
 ORGANISM: Saccharomyces cerevisiae US-10-084-700-28
 US-10-084-700-28
 TYPE: PRT
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 61 D-CAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDAPIRCVEY--CPEVNVMVTGSWD 117
 91 DVCWSDDGSKVFTASCDKTAKWWDLSSNQAIQIAQHDAPVKTIHWIKAPWYSCVWTGSWD 150
 151 KTLKFWDTRSSNPMMVLQLPERCYCADVIYPMAVVATAERGLIVYQLENQPSBFRRIESP 210
 118 QTVKLMDPRIPCNAGTESQPEKVYTLSVSGDRLIVGTAGRRVLVWDLRNMGYVQQRRESS 177
 178 LKYQTRCIRAFPNKQ----GYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNI-- 231
 232 -EQIYPVNAISFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTT 290
 270 PQDIYAVNGIAFHPVHGTLAIVGSDGRESFWDKDARIKLKISBQLDQPISACCFNHNGNI 329
 9
 31 DIEVTSSPDDSIGCLSFSPPTLPGNPLIAGSWANDVRCWEVODSGQTIPKAQQMHTGPVL 90
 6 EFKLNQPPEDGISSVKFSPNT--SQFLLVSSWDISVRLYDVPANSM---RLKYQHTGAVL
 Query Match
29.7%; Score 509; DB 14; Length 368;
Best Local Similarity 34.3%; Pred. No. 2.18-45;
Best Local Similarity 34.3%; Mismatches 116; Conservative 61; Mismatches 141; Indels 20
 Sequence 712, Application Us/09925302
| Reach No. 1920-2004441A1
| Reach No. 1920-2004441A1
| Repented No. 1920-2004441A1
| THILL OF INVESTIGATION IN LILE OF INVESTIGATION IN LILE REPERRICE: PAIG 401-08-10
| THILL OF INVESTIGATION NUMBER: US/09/925,302
| CURRENT FALTAN DATE: 2001-08-10
| PRIOR FILIND DATE: 2001-08-10
| PRIOR FILIND DATE: 1999-03-12
| ROSA PPLICATION UNMERS 60/124,270
| ROSA PPLICATION UNMERS 60/124,270
| ROSA PPLICATION UNMERS 60/124,270
| ROSA PRICE REACHION UNCS: 956
| SOFTHARE PRICE ROLLING PRICE REACHION
 PROPERTY SERVICE TO A TAPPLICATION US/10084700.
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CURRENT APPLICATION UNMERR US/10/034,700
CURRENT APPLICATION UNMERR US/10/034,700
CURRENT PRINCE ADD NOS: 302-02-27
NUMBER OF SEC ID NOS: 32
SOFTAARE: FastSED for Windows Version 4.0
SOFTAARE: 308
 291 LAIASSYMYEMDD---TEHPEDGIFIRQVTDAETKPKS 325
 330 FAYASSYDWSKGHEFYNPOKKNYIFLRNAAE-ELKPRN 366
319 WSKGYTFNNAQLP-NKIMLHPVPQDBIKPR 347
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-712
 , ORGANISM: Homo sapien
US-10-084-700-30
 US-09-925-302-712
 US-10-084-700-30
 TYPE: PRT
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 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KER: SITE
COCATION: (23)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (23)
OTHER HUNGNATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
 LOCATION: (18)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (43)
OTHEN THORATION: Xaa equals any of the naturally occurring L-amino acids
MANB/KRY: STRE
 LOCATION: (48)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KBY: SITE
 LOCATION: (49)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (89)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1045
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KBY: SITE
 LOCATION: (91)
OTHER INFORMATION: Xaa equals any of the natuxally occurring L-amino acids
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LOCATION: 13)
OTHER INFORMATION: Xea equals amy of the naturally occurring L. amino acids
 1, Gaps
 44 VPANSMRLKYQHTGAVLDCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDA 97
 24 VPANSMRLKYQHTGXVLDCXFYGPXXAWSXGLDHQLKMHDL-TLIKKISWTHXA 76
 Ouery Match
11.14, Score 197.5; DB 9; Length 100;
Best Local Similarity 72.28; Fred. No. 4.5e-13,
Matches 39; Conservative 2; Mismarches 12, Indels 1,
Matches 39; Conservative 2; Mismarches 12,
 Sequence 1045. Application US/09922299
GENERAL GROWN US/09922299
GENERAL GROWN US/09925090
GENERAL GROWN US/09925090
TILTE OF INVENTION NAMES: US/09/925,299
CURRENT PAPLICATION NAMES: US/09/925,299
RAIGN FARLENG NATE: 2001-08-10-978299
RRIOR FILING DATE: 2001-08-10-978299
RRIOR FILING DATE: 2000-09-06
RRIOR FILING DATE: 1999-00-12
NUMBER FOR FILING DATE: 1999-00-12
NUMBER OF SEQ ID NOS: 1856
SEQ ID NOS: 1856
SEQ ID NOS: 1856
LENGTH NO 1046
 ORGANISM: Homo sapiens
 NAME/KEY: SITE
LOCATION: (53)
 NAME/KEY: SITE
LOCATION: (78)
 NAME/KEY: SITE
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 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
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 GENERAL INCOMMENTION: A CONTROL OF CONTROL O
 MRLKYQHTGAVLDCAFYDPTHAWSGGLDHQLKKHDLNTDQENLVGT 46
 49 MRLKYQHTGAVLDCAFYDPTHAWSGGLDHQLXMHDLNTDQENLVGT 94
 0; Indels
281 QTRKKIKNFAKFNEDSVVKIACSDN--ILCLATS-----DDT 315
 Query Match 14.6%; Score 258; DB 12; Best Local Similarity 100.0%; Pred. No. 7.4e-20; Marches 46; Conservative 0; Mismatches 0;
 Sequence 1045, Application US/09925299
Patent No. US20020055627A1
 Sequence 157, Application US/09903190 Publication No. US20030162176A1 GENERAL INFORMATION:
 ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 NAME/KEY: SIGNAL
; LOCATION: -22..-1
US-09-903-190-157
 US-09-925-299-1045
 TYPE: PRT
 SEQ ID NO 1045
 FEATURE:
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73 GGLDHQLKMHDLNTDQENLV-GTHDAPIRCVEYCPEVNVMVTGSWDOTVKLWDPRTPCNA 131
 132 GTFSQP-EKVYTLSVSGD-RLIVGTAGRRVLVWDLRNMGYVQQRRESSLKYQTRCIRAFP 189
 190 -NKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISFHNIHNT 248
 676 PSPDGALLASGSDDRIIRLWDVAAQEE------HTTLEGHTE---PVHSVAFHPEGTT 724
 15 DGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQ-HTGAVLDCAFY-DPTHAWS 72
 Gaps
 23;
 OTHER INFORMATION: amino acid sequence encoded by the PKWA gene
 DB 14; Length 742;
 Query Match 11.1%; Score 197.5; DB 14; Length : Best Local Simlarity 27.7% Pred. No. 8.8e-12; Indels Matches 70; Conservative 48; Mismatches 112; Indels
 PATHE OF INVENTION TO TRASE-ASSOCIATED PROTEINS NUMBER OF SEQUENCES 6 CORRESPONDENCE ADDRESS:
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Mindows Version 3.0
 ATTORNEY/AGENT INPORVATION:
NAME: David G. Streeter
REGISTRATION NUMBER: 43,168
REFERENCE/DOCKET NUMBER: PF-0508-1 DIV
TELECOMMUNICATION: INFORMATION:
 APPLICATION NUMBER: US/09/590,540
FILING DATE: 08-2/Un-2003
APPLICATION NUMBER: 09/063,743
FILING DATE: April 21, 1998
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/119,932
FILING DATE: 09-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
 ADDRESSEE: Incyte Genomics, Inc.
STREET: 3160 Porter Drive
 Sequence I, Application US/10119932
Publication No. US2002016048BA1
GENERAL INFORMATION:
APPLICANT: Bandman, olga
ORGANISM: Thermomonospora curvata
 Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
 TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
 STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
 249 FATGGSDGFVNIW 261
 725 LASASEDGTIRIW 737
 CITY: Palo Alto
 US-10-077-111-11
 RESULT 15
US-10-119-932-1
 FEATURE:
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 LOCATION: (16)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEX: SITE
 LOCATION: (23)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (75)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1045
 Gaps
 44 VPANSMRLKYQHTGAVLDCAFYDPTHAWSGGLDHQLKMHDLNTDQENLVGTHDA 97
 1,
 Query Match 11.1%; Score 197.5; DB 11; Length 100; Bet Local Similarity 72.2%; Pred. No. 45-13; Metches 39; Conservative 2; Mismatches 12; Indels 1;
 APELCANT: Todderud, C. Gordon
APELCANT: Finger, Joshua N.
APELCANT: Finger, Johna N.
APELCANT: Finger, Johna N.
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APELCANT: Finger, Johna N.
APELCANT: Finger, Johna N.
APELCANT: Finger, Johna N.
APELCANT: PAPELCATION NUMBER: 60/1994,181
RNOR FILING DATE: Z001-06-29
RNOR FILING DATE: Z001-06-29
RNOR FILING DATE: Z001-02-16
RNOR FILING DATE: Z001-02-16
RNOR PRICE OF SEQ ID NOSE: 25
SOFTWARE: PAREIT NUMBER: 62/189
 Sequence 11, Application US/10077111
Publication No. US20020187492A1
GENERAL INFORMATION:
 NAME/KEY: SITE
LOCATION: (43)
 NAME/KEY: SITE
 WAME/KEY: SITE
 LOCATION: (19)
 LOCATION: (38)
 LOCATION: (99)
 US-10-077-111-11
 LOCATION:
 LOCATION:
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 LOCATION:
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Matches
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66 BGEVYCCKFHPNGST-LASAGFDRLILLMNVYGDCDNYATLK-GHSGAVMELHYNTDGSM 123
 70 AWSGGLDHQLKWHDLNTDQ--ENLVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRT 127
 124 LFSASTDKTVAVMDSETGERVKRLKGHTSFVNSCYPARRGPQLVCTGSDDGTGKLMDIRK 183
 128 PCNAGTĘSQPEKY--YŢLSVSGDRLĮVGTAGRRVLVWDLRNMGYVQQRKESSLKYQTŖ-- 183
 184 KAAIQTEQNIYQVLAVTENDTSDQIISGGIDNDIXVWDL------RQNKLTYTMRGH 234
 184 ----CIRAFPNKQGYVLSSIEGRVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNA 239
 235 ADSVTGLSLSSEGSYLLSNAMDN-TVRVMDVRFFAPKE----RCVKIFQGNVHN-FEKNL 288
 240 I -- SFHNIHNTFATGGSDGFVNIWDPFNKKRLCQFHRYPTSIASLAFSNDGTTLAIASS- 296
 : | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; |
 14 EDGISSVKFSPNTSOPLLVSSWDTSVRLYDVPA---NSMRLKYQHTGAVLDCAF-YDPTH 69
 Ouery March 10.0%; Score 176.5; DB 14; Length 375; Bost Local Similarity 25.8%; Pred. No. 5:5-01. Indels 37; Gaps Marches 90; Conservative 51; Mismatches 142; Indels 37; Gaps
TYPE: anino acids
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TYPE: alion
 Search completed: November 12, 2003, 20:12:03 Job time : 31 secs
 349 KRLYMGEFSE 358
 297 ---YMYENDD 303
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